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NEWS 26 PCTFUL now contains images
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NEWS 28 EVENTLINE will be removed from STN
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NEWS 30 Additional information for trade-named substances without
structures available in REGISTRY
NEWS 31 Display formats in DGENE enhanced
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NEWS 35 New current-awareness alert (SDI) frequency in
WPIDS/WPINDEX/WPIX
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added to PHAR
NEWS 38 MEDLINE file segment of TOXCENTER reloaded
NEWS 39 Supporter information for ENCOMPAT and ENCOMPULIT updated
NEWS 40 CHEMREACT will be removed from STN
NEWS 41 Simultaneous left and right truncation added to WSCA
NEWS 42 RAPPA enhanced with new search field, simultaneous left and
right truncation
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L1 8 FILES SEARCHED .. 1
L1 151 MORE (A) 1
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L2 100 DUP REM L1 (51 DUPLICATES REMOVED)
=> s 12 not py=>1995

'1995, NOT A VALID FIELD CODE
5 FILMS SEARCHED...
L3 10 L2 NOT PY=>1995

=> d 1-10

L3 ANSWER 1 OF 10 MEDLINE
AN 80137745 MEDLINE
DN 80137745 Pubmed ID: 536396
TI (Sub-phrenic abscess: 28 cases, one death (author's trans1)).
AU Abcex sous-phreniques. 28 observations: 1 mort.
SO Counaud C
JOURNAL DE CHIRURGIE. (1979 Aug-Sep) 116 (8-9) 481-5.
CY Journal code: 0374754. ISSN: 0021-7697.
DT France
LA Journal: Article: (JOURNAL ARTICLE)
FS French
EM Priority Journals
ED 198005
Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19800514

L3 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2003 ACS
AN 1983:594018 CAPLUS
DN 99:194018
TI Comment on the comment of Dr. W. Gruendler on the paper "Heats of atomization of conjugated hydrocarbons by a new semiteoretical method"
AU Zivovoyc, Tomislav P.
CS "Rudjer Boskovic" Inst., Zagreb, YU-41001, Yugoslavia
SO Theoretica Chimica Acta (1983), 63(5), 443-4
CODEN: TCHAMM; ISSN: 0040-5744
DT Journal
LA English

L3 ANSWER 3 OF 10 USPATFULL
AN 93:102800 USPATFULL
TI Substituted semicarbazone arthropodicides
IN Daut, John P., Wilmington, DE, United States
TI Lahm, George P., Wilmington, DE, United States
PA Marlin, Bradford S., Cochranville, PA, United States
PA E. I. Du Pont de Nemours and Company, Wilmington, DE, United States
PI (U.S. corporation)
AI US 5268388
PI 19931207
AI 19921102 (7)
AI Division of Ser. No. US 1991-689042, filed on 20 May 1991, now patented.
AI Pat. No. US 5182303 which is a continuation-in-part of Ser. No. US 1989-436361, filed on 13 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1988-290404, filed on 27 Dec 1988, now abandoned
DT Utility
FS Granted
LN.CNT 3597
INCL INCLM: 514/470.000
INCL 514/080.000; 514/096.000; 514/100.000; 514/415.000; 514/443.000;
544/143.000; 546/196.000; 548/483.000; 548/111.000; 549/053.000;
549/055.000; 549/057.000; 549/466.000; 549/467.000; 549/006.000;
549/220.000
NCLM: 514/470.000
NCL 514/080.000; 514/096.000; 514/100.000; 514/415.000; 514/443.000;
544/143.000; 546/196.000; 548/111.000; 548/483.000; 549/053.000;
549/055.000; 549/057.000; 549/466.000; 549/467.000; 549/220.000;
549/466.000;
549/467.000
IC (5)
ICM: A61K031-34

ICS: A61K031-38; C07D367-82; C07D333-66
EXP 549/53; 549/55; 549/57; 549/466; 549/467; 549/6; 549/220; 549/113;
548/983; 544/143; 546/196; 514/80; 514/96; 514/100; 514/415; 514/443;
514/470

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 4 OF 10 USPATFULL
AN 93:7135 USPATFULL
TI Substituted semicarbazone arthropodicides
IN Daut, John P., Wilmington, DE, United States
TI Lahm, George P., Wilmington, DE, United States
PA Marlin, Bradford S., Cochranville, PA, United States
PA E. I. Du Pont de Nemours and Company, Wilmington, DE, United States
PI (U.S. corporation)
AI US 5182303
AI US 1991-689042
AI WO 1989-US5597
19930126
19910520 (7)
19891220

RLI Continuation-in-part of Ser. No. US 1989-436361, filed on 13 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1988-290404, filed on 27 Dec 1988, now abandoned
DT Utility
FS Granted
LN.CNT 358
INCL INCLM: 514/583.000
INCL 514/530.000; 514/521.000; 514/588.000; 558/404.000; 560/028.000;
560/034.000; 564/020.000; 564/021.000; 564/036.000
NCLM: 514/583.000
NCL 514/521.000; 514/530.000; 514/588.000; 558/404.000; 560/028.000;
560/034.000; 564/020.000; 564/021.000; 564/036.000
IC (5)
ICM: A01N047-34
ICS: A01N047-30; C07C281-12; C07C337-08
EXP 564/20; 564/21; 564/36; 514/583; 514/588
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 10 USPATFULL
AN 89:80818 USPATFULL
TI Multicidal composition
IN Gorman, George S., Saanichton, Canada
IN Gorman, Michelle D., Victoria, Canada
PA Safer, Inc., Newton, MA, United States (U.S. corporation)
AI US 4870102
AI US 1988-182137
AI 19890926
AI 19880415 (7)
DT Utility
FS Granted
LN.CNT 286
INCL INCLM: 514/493.000
INCL 514/560.000
NCLM: 514/493.000
NCL 514/560.000
IC (4)
ICM: A01N055-04
ICS: 514/493; 514/560
EXP 514/493; 514/560
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 6 OF 10 USPATFULL
AN 86:59257 USPATFULL
TI Quarantine system for papaya
IN Covey, H. Melvin, Hilo, HI, United States
IN Hayes, Charles F., Kailua, HI, United States
PA The United States of America as represented by the Secretary of Agriculture, Washington, DC, United States (U.S. government)
PA The University of Hawaii, Honolulu, HI, United States (U.S. corporation)

PI US 4618497 19861021
 AI US 1985-757396 19850722 (6)
 DT Utility
 FS Granted
 LN CNT 1458
 INCL INCLM: 426/233.000
 INCLM: 426/615.000; 426/521.000
 NCL INCLM: 426/233.000
 NCLM: 426/233.000
 NCLS: 426/521.000; 426/615.000
 IC [4]
 ICM: A23L001-212
 426/615; 426/438; 426/418; 426/419; 426/509; 426/520; 426/231; 426/232;
 426/233; 426/521
 EXF
 L3 ANSWER 7 OF 10 USPTFULL
 AN 86:23427 USPTFULL
 TI Pesticidal compositions
 IN Debeck, Jozeff, Oberwilt, Switzerland
 Lege, John, Witterwilt, Switzerland
 Bachmann, Markus, Riehn, Switzerland
 PA Ciba-Geigy Corporation, Ardsley, NY, United States (U.S. corporation)
 PI US 4584296 19860422
 PI US 1984-612236 19840521 (6)
 PRAI CH 1983-2942 19830530
 CH 1983-297 19830503
 CH 1983-2944 19830503
 DT Utility
 FS Granted
 LN CNT 273
 INCL INCLM: 514/147.000
 INCLM: 514/147.000
 NCL INCLM: 514/147.000
 NCLM: 514/147.000
 NCLS: 514/346.000
 IC [4]
 ICM: A01N057-10
 ICS: A01N043-40
 EXF 424/225; 424/324; 424/263; 514/147; 514/346
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 L3 ANSWER 8 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1994021905 PCTFULL ED 20020513
 TIEN IMPROVEMENTS TO COMPRESSION OR SPARK IGNITION FOUR-STROKE INTERNAL
 COMBUSTION ENGINES HAVING A VARIABLE COMPRESSION RATIO ENABLING HIGH
 SUPERCHARGING PRESSURE LEVELS
 TIFR PERFECTIONNEMENTS APPORTES AUX MOTEURS A COMBUSTION INTERNE A QUATRE
 TEMPS A RAPPORT VOLUMETRIQUE VARIABLE AUTORISANT DE HAUTS TAUX DE
 PRESSIONS DE SURALIMENTATION ET FONCTIONNANT PAR ALLUMAGE PAR
 COMPRESSION OU PAR ALLUMAGE COMMANDE
 IN VAN AVERMAETE, Gilbert, Lucien, Charles, Henri, Louis
 PA VAN AVERMAETE, Gilbert, Lucien, Charles, Henri, Louis
 LA French
 DT Patent
 PI WO 9421905 AI 19940929
 W: AU BR CA CN CZ JP RU US AT BE CH DE DK ES FR GB GR IE IT LU
 MC NL PT SE
 AI 19940321
 PRAI LU 1993-88235 A 19930319
 ICM F02B041-00
 ICS F02D015-04
 L3 ANSWER 9 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1991007382 PCTFULL ED 20020513
 TIEN SUBSTITUTED SEMICARBAZONE ARTHROPODICIDES
 TIFR ARTHROPODICIDES A BASE DE SEMICARBAZONES SUBSTITUES
 DAUB, John, Powell;

LAM, George, Philip;
 MARLIN, Bradford, Senn
 E.I. DU PONT DE NEMOURS AND COMPANY
 PA English
 LA Patent
 DT Patent
 PI WO 9107382 JP KR AI 19910530
 W: WO 1990-US3347 A 19900620
 AI US 1989-436,361 19891113
 PRAI US 1989-PT/US89/05597 19891220
 ICS A01N047-34
 L3 ANSWER 10 OF 10 PCTFULL COPYRIGHT 2003 Univentio
 AN 1985002768 PCTFULL ED 20020507
 TIEN NEW THERAPEUTICAL APPLICATION OF AN INDIANE DIONE DERIVATIVE AND
 PHARMACEUTICAL COMPOSITIONS INTENDED TO SAID UTILIZATION
 TIFR NOUVELE APPLICATION THERAPEUTIQUE D'UN DERIVE DE L'INDIANE DIONE ET LES
 COMPOSITIONS PHARMACEUTIQUES DESTINEES A CET USAGE
 IN PETIBON, Guy
 PA LABORATOIRES BOUCHARD;
 PETIBON, Guy
 LA French
 DT Patent
 PI WO 8502768 AI 19850704
 DS W: AT AU BE CH DE DK FI FR GA GB HU JP KR LU ML MR NL
 NO SE SN TD TG US
 AI WO 1984-FR302 A 19841224
 PRAI FR 1983-83/20755 19831226
 ICM A61K031-12
 ICS C07C049-84
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 4471 FADD OR FAS (A) ASSOCIATED (A) DEATH (A) DOMAIN
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 8 FILES SEARCHED...
 L6 => dup rem 15
 PROCESSING COMPLETED FOR L5
 354 DUP REM L5 (2 DUPLICATES REMOVED)
 L7 => s 16 not PY=>1995
 1995 NOT A VALID FIELD CODE
 6 FILES SEARCHED...
 L7 0 L6 NOT PY=>1995
 =>
 => d 1-10 16
 L6 ANSWER 1 OF 354 USPTFULL
 AN 2003:159813 USPTFULL
 TI Novel molecules of the card-related protein family and uses thereof
 IN Berlin, John, Watertown, MA, UNITED STATES
 PI US 2001-109428 AI 200103612
 AI US 2001-798412 AI 20010302 (9)
 RLI Continuation-in-part of Ser. No. US 2000-728260, filed on 1 Dec 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-685791, filed on 10
 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-513904, filed
 on 25 Feb 2000, PENDING Continuation-in-part of Ser. No. US 2000-507533,
 filed on 18 Feb 2000, PENDING
 PRAI US 1999-168780P 19991201 (60)
 DT Utility

FS APPLICATION
LN CNT 5413
INCL INCL: 514/012.000
INCL: 435/006.000; 435/320.100; 435/194.000; 435/325.000; 435/069.100;
536/023.200; 530/388.260
NCL NCLM: 514/012.000
NCL: 435/006.000; 435/320.100; 435/194.000; 435/325.000; 435/069.100;
536/023.200; 530/388.260
IC [7]
ICM: A61K038-17
ICS: C12N001-68; C07H021-04; C12N009-12; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 2 OF 354 USPTAFULL
AN 2003:159379 USPTAFULL
TI Identification of a novel domain in the tumor necrosis factor receptor
IN family that mediates pre-ligand receptor assembly and function
Lenardo, Michael J., Bethesda, MD, UNITED STATES
Chen, Francis Ka-Ming, Silver Spring, MD, UNITED STATES
Siegel, Richard M., Washington, DC, UNITED STATES
PI US 2003:108992 A1 2003:0612
US 2002-203495 A1 2002:0809 (10)
WO 2001-US4125 2001:0209
DT Utility
FS APPLICATION
LN CNT 2206
INCL INCLM: 435/069.100
INCL: 435/320.100; 435/325.000; 530/350.000; 536/023.500
NCLM: 435/069.100
NCL: 435/320.100; 435/325.000; 530/350.000; 536/023.500
IC [7]
ICM: C07K014-715
ICS: C07H021-04; C12P021-02; C12N005-06

L6 ANSWER 3 OF 354 USPTAFULL
AN 2003:153330 USPTAFULL
TI Secreted and transmembrane polypeptides and nucleic acids encoding the
IN same
Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
Baker, Kevin P., Darnestown, MD, UNITED STATES
Botstein, David, Belmont, CA, UNITED STATES
Desnoyers, Luc, San Francisco, CA, UNITED STATES
Eaton, Dan L., San Rafael, CA, UNITED STATES
Ferrara, Napoleone, San Francisco, CA, UNITED STATES
Filvaroff, Ellen, San Francisco, CA, UNITED STATES
Fong, Sherman, Alameda, CA, UNITED STATES
Gerber, Hanspeter, San Francisco, CA, UNITED STATES
Gertsen, Mary E., San Mateo, CA, UNITED STATES
Goddard, Audrey, San Francisco, CA, UNITED STATES
Grodowski, Paul J., Burlingame, CA, UNITED STATES
Grimaldi, J. Christopher, San Francisco, CA, UNITED STATES
Gurney, Austin L., Belmont, CA, UNITED STATES
Hillman, Kenneth J., San Francisco, CA, UNITED STATES
Kljasin, Ivar J., Lafayette, CA, UNITED STATES
Kuo, Sophia S., San Francisco, CA, UNITED STATES
Napier, Mary A., Hillsborough, CA, UNITED STATES
Pan, James, Belmont, CA, UNITED STATES
Paoni, Nicholas F., Belmont, CA, UNITED STATES
Roy, Margaret Ann, San Francisco, CA, UNITED STATES
Shelton, David L., Oakland, CA, UNITED STATES
Stewart, Timothy A., San Francisco, CA, UNITED STATES
Tumas, Daniel, Orinda, CA, UNITED STATES
Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
Wood, William I., Hillsborough, CA, UNITED STATES

PA Genentech, Inc. (U.S. corporation)
PI US 2003:104998 A1 2003:0605
AI US 2001-978643 A1 2001:1016 (9)
RLI

Continuation of Ser. No. US 1998-40220, filed on 17 Mar 1998, GRANTED, Pat. No. US 6391311 Continuation of Ser. No. US 1998-105413, filed on 26 Jun 1998, ABANDONED Continuation of Ser. No. US 1998-168978, filed on 7 Oct 1998, ABANDONED Continuation of Ser. No. US 1998-184216, filed on 2 Nov 1998, ABANDONED Continuation of Ser. No. US 1998-187368, filed on 6 Nov 1998, PENDING Continuation of Ser. No. US 1998-202054, filed on 7 Dec 1998, PENDING Continuation of Ser. No. US 1998-218517, filed on 22 Dec 1998, ABANDONED Continuation of Ser. No. US 1999-254465, filed on 5 Mar 1999, GRANTED, Pat. No. US 6410708 Continuation of Ser. No. US 1999-265686, filed on 10 Mar 1999, GRANTED, Pat. No. US 6455283 Continuation of Ser. No. US 1999-267213, filed on 12 Mar 1999, ABANDONED Continuation of Ser. No. US 1999-284291, filed on 12 Apr 1999, ABANDONED Continuation of Ser. No. US 1999-311832, filed on 14 May 1999, PENDING Continuation of Ser. No. US 1999-318017, PENDING Continuation of Ser. No. US 1999-380138, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US 1999-380142, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US 2000-709238, filed on 8 Nov 2000, ABANDONED Continuation of Ser. No. US 2000-723749, filed on 27 Nov 2000, PENDING Continuation of Ser. No. US 2000-747259, filed on 20 Dec 2000, PENDING Continuation of Ser. No. US 2001-816744, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US 2001-816920, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US 2001-854280, filed on 10 May 2001, PENDING Continuation of Ser. No. US 2001-854208, filed on 10 May 2001, PENDING Continuation of Ser. No. US 2001-872035, filed on 1 Jun 2001, ABANDONED Continuation of Ser. No. US 2001-874503, filed on 5 Jun 2001, PENDING Continuation of Ser. No. US 2001-882636, filed on 5 Jun 2001, ABANDONED Continuation of Ser. No. US 2001-886342, filed on 19 Jun 2001, ABANDONED Continuation of Ser. No. US 2001-918585, filed on 30 Jul 2001, PENDING

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US 1998-113621P 19981223 (60)
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US 1999-126773P 19990329 (60)
US 1999-130232P 19990421 (60)
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US 1999-139557P 19990616 (60)
US 1999-141037P 19990623 (60)
US 1999-142680P 19990707 (60)
US 1999-145698P 19990726 (60)
US 1999-146222P 19990728 (60)
US 1999-162506P 19991029 (60)

DT
FS
APPLICATION
UTILITY

IN.CNT 21741
INCL INCLM: 514/012.000

INCL INCLM: 530/388.100; 536/023.200; 435/006.000; 435/069.100;
435/007.100; 435/325.000; 435/320.100

NCL INCLM: 514/012.000
NCLM: 530/350.000; 530/388.100; 536/023.200; 435/006.000; 435/069.100;
435/007.100; 435/325.000; 435/320.100

IC [7]
ICM: A61K038-17

ICS: C12Q001-68; G01N033-53; C07H021-04; C12P021-02
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 4 OF 354 USPATFULL
AN 2003:152892 USPATFULL

TI Secreted and transmembrane polypeptides and nucleic acids encoding the same

IN Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
 Baker, Kevin P., Darnestown, MD, UNITED STATES
 Botstein, David A., Belmont, CA, UNITED STATES
 Desnoyers, Luc, San Francisco, CA, UNITED STATES
 Eaton, Dan L., San Rafael, CA, UNITED STATES
 Ferrara, Napoleone, San Francisco, CA, UNITED STATES
 Fong, Wei-Qiang, Alameda, CA, UNITED STATES
 Gerber, Hanspeter, San Francisco, CA, UNITED STATES
 Gerltzen, Mary E., San Mateo, CA, UNITED STATES
 Goddard, Audrey, San Francisco, CA, UNITED STATES
 Godowski, Paul J., Hillsborough, CA, UNITED STATES
 Gurney, Austin L., Belmont, CA, UNITED STATES
 Kijavini, Ivar J., Lafayette, CA, UNITED STATES
 Mather, Jennie P., Millbrae, CA, UNITED STATES
 Napier, Mary A., Hillsborough, CA, UNITED STATES
 Pan, James, Belmont, CA, UNITED STATES
 Paoni, Nicholas F., Belmont, CA, UNITED STATES
 Roy, Margaret Ann, San Francisco, CA, UNITED STATES
 Stewart, Timothy A., San Francisco, CA, UNITED STATES
 Tumas, Daniel, Orinda, CA, UNITED STATES
 Watanabe, Colin K., Moraga, CA, UNITED STATES
 Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
 Wood, William I., Hillsborough, CA, UNITED STATES
 Zhang, Zemin, Foster City, CA, UNITED STATES

PA Genentech, Inc. (U.S. corporation)
 PI US 2003104558 AI 20030605
 RLI US 2002-226739 AI 20020823 (10)
 Continuation of Ser. No. US 2001-2796, filed on 15 Nov 2001, PENDING
 PRAI Continuation of Ser. No. US 2000-0514042, filed on 22 May 2000, PENDING

PA US 1999-052011 19990901
 WO 1999-US20594 19990908
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 WO 1999-US21547 19990915
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 WO 2001-US21735 20010709
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DT US 1999-149396P 19990817 (60)
 US 1999-169495P 19991207 (60)
 FS Utility
 IN CNT 11726
 INCL INCLM: 435/069.100
 INCLM: 435/183.000; 435/320.100; 435/325.000; 530/350.000; 536/023.200
 NCLM: 435/069.100
 NCLM: 435/183.000; 435/320.100; 435/325.000; 530/350.000; 536/023.200
 IC [7]
 ICM: C12P021-02
 ICS: C12N005-06; C07K014-435; C07H021-04; C12N009-00
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 5 OF 354 USPATFULL
 AN 2003152870 USPATFULL
 TI Secreted and transmembrane polypeptides and nucleic acids encoding the same

IN Ashkenazi, Avi J., San Mateo, CA, UNITED STATES
 Baker, Kevin P., Darnestown, MD, UNITED STATES
 Botstein, David, Belmont, CA, UNITED STATES
 Desnoyers, Luc, San Francisco, CA, UNITED STATES
 Eaton, Dan L., San Rafael, CA, UNITED STATES
 Ferrara, Napoleone, San Francisco, CA, UNITED STATES
 Fong, Sherman, Alameda, CA, UNITED STATES
 Gao, Wei-Qiang, Palo Alto, CA, UNITED STATES
 Gerber, Hanspeter, San Francisco, CA, UNITED STATES
 Gerltzen, Mary E., San Mateo, CA, UNITED STATES
 Goddard, Audrey, San Francisco, CA, UNITED STATES
 Godowski, Paul J., Burlingame, CA, UNITED STATES
 Girmaidi, J. Christopher, San Francisco, CA, UNITED STATES
 Gurney, Austin L., Belmont, CA, UNITED STATES
 Hillan, Kenneth J., San Francisco, CA, UNITED STATES
 Kijavini, Ivar J., Lafayette, CA, UNITED STATES
 Kuo, Sophia S., San Francisco, CA, UNITED STATES
 Napier, Mary A., Hillsborough, CA, UNITED STATES
 Pan, James, Belmont, CA, UNITED STATES
 Paoni, Nicholas F., Belmont, CA, UNITED STATES
 Roy, Margaret Ann, San Francisco, CA, UNITED STATES
 Shelton, David L., Oakland, CA, UNITED STATES
 Stewart, Timothy A., San Francisco, CA, UNITED STATES
 Tumas, Daniel, Orinda, CA, UNITED STATES
 Watanabe, Colin K., Moraga, CA, UNITED STATES
 Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
 Wood, William I., Hillsborough, CA, UNITED STATES

PA Genentech, Inc. (U.S. corporation)
 PI US 2003104536 AI 20030605
 RLI US 2001-166709 AI 20011019 (10)
 Continuation of Ser. No. US 2001-918585, filed on 30 Jul 2001, PENDING
 PRAI Continuation of Ser. No. US 2001-918585, filed on 30 Jul 2001, PENDING

PA US 1998-US21141 19981007
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Tunas, Daniel, Orinda, CA, UNITED STATES
Williams, P. Mickey, Half Moon Bay, CA, UNITED STATES
Wood, William I., Hillsborough, CA, UNITED STATES
PA Genentech, Inc. (U.S. corporation)
PI US 2000096744 AI 20010522
AI US 2002-978187 AI 20020128 (9)

Continuation of Ser. No. US 2001-918585, filed on 30 Jul 2001, PENDING
Pat. No. US 6391111 Continuation of Ser. No. US 1998-40220, filed on 17 Mar 1998, GRANTED
Jun 1998, ABANDONED Continuation of Ser. No. US 1998-105413, filed on 26
Oct 1998, ABANDONED Continuation of Ser. No. US 1998-168978, filed on 7
Nov 1998, ABANDONED Continuation of Ser. No. US 1998-184216, filed on 2
Nov 1998, ABANDONED Continuation of Ser. No. US 1998-187368, filed on 6
Dec 1998, PENDING Continuation of Ser. No. US 1998-202054, filed on 7
Dec 1998, ABANDONED Continuation of Ser. No. US 1998-218517, filed on 22
Mar 1999, GRANTED, Pat. No. US 6410708 Continuation of Ser. No. US
1999-265686, filed on 10 Mar 1999, GRANTED, Pat. No. US 6455283
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Continuation of Ser. No. US 1999-284291, filed on 12 Apr 1999, ABANDONED
Continuation of Ser. No. US 1999-311832, filed on 14 May 1999, PENDING
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1999-380138, filed on 25 Aug 1999, ABANDONED Continuation of Ser. No. US
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2000-723749, filed on 27 Nov 2000, ABANDONED Continuation of Ser. No. US
2000-747259, filed on 20 Dec 2000, PENDING Continuation of Ser. No. US
2001-816744, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-816920, filed on 22 Mar 2001, PENDING Continuation of Ser. No. US
2001-854280, filed on 10 May 2001, PENDING Continuation of Ser. No. US
2001-854208, filed on 10 May 2001, PENDING Continuation of Ser. No. US
2001-872035, filed on 1 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-874503, filed on 5 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-882636, filed on 19 Jun 2001, ABANDONED Continuation of Ser. No. US
2001-886342, filed on 14 Jun 2001, ABANDONED

PRAI WO 1998-US21141 19981107
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US 1999-145698P 19990726 (60)
US 1999-146222P 19990728 (60)
US 1999-162506P 19991029 (60)

DT
Utility
FS
APPLICATION
LN.CNT 21776
INCL INCLM: 514/012.000; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
INCLM: 435/069.100; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
NCLM: 514/012.000
NCLM: 514/012.000; 435/320.100; 435/183.000; 435/325.000; 530/350.000;
NCLM: 536/023.200
IC (7)
ICM: A61K038-17
ICS: C12P021-02; C12N005-06; C07H014-435; C07H021-04; C12N009-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 10 OF 354 USPATFUL
AN 2003:140406 USPATFUL
TI Human CDNA's and proteins and uses thereof
IN Bejanin, Stephane, Paris, FRANCE
Tanaka, Hiroaki, Antony, FRANCE
PA GENSET, S.A., Paris, FRANCE, 75008 (non-U.S. corporation)
PI US 2003/096247 AI 20030522
AI US 2001-986 AI 20011114 (10)
RLI Division of Ser. No. US 2001-924340, filed on 6 Aug 2001, PENDING
PRAI WO 2001-181715 20010806
US 2001-305456P 20010713 (60)
US 2001-302277P 20010629 (60)
US 2001-298698P 20010615 (60)
US 2001-293574P 20010525 (60)

DT
Utility
FS
APPLICATION
LN.CNT 2566
INCL INCLM: 435/006.000
INCLM: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
INCLM: 435/023.200; 800/008.000
NCLM: 435/006.000
NCLM: 435/069.100; 435/183.000; 435/320.100; 435/325.000; 530/350.000;
IC (7)
ICM: C12N001-68
ICS: A01K067-00; C07H021-04; C12N009-00; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L6 ANSWER 10 OF 354 USPATFUL
DETD . . . a contiguous surface of the native conformation of a polypeptide of the present application. Additionally, the antibody is capable of binding a nonlinear epitope presented by a synthetic peptide designed to mimic a contiguous surface of the native conformation of a polypeptide of a sequence selected from the group. . . use in caspase-dependent cell death including incubation of carcinoma cells with compositions comprising polypeptides of preferred sequences comprising RLAWGDRDNKIMDEDES and PAD DED-related domains as described in Ederstadt, et al., Nature, 392:941-945, 1998, and Hackam, et al., J Biol Chem, 275:41299-41308, 2000, which disclosures are hereby. . . effector domain RLAWGDRDNKIMDEDES, and the death effector domain of the huntingtin-interacting protein (HIP-1), conserved among related sequences with the consensus peptide SSYRLRLILSELSSELEVLFLCNDIPKRLKLTALDLSALEEGCLISEDNLSLAE LYLRLRLDLRLRFG for competitive binding studies with wild-type huntingtin and the disease-causing mutant. By contacting polypeptides of the invention with wt- and mt- (glutamine-rich) huntingtin. . . sulfated glycosaminoglycans covalently bound to core protein. The ability to bind heparin-like moieties includes RFGs within the more encompassing Heparin Binding Growth Factor (HBGF) superfamily; of peptide growth factors. Additionally, RFGs bind the cysteine-rich FGF-R (cFR), an integral single transmembrane protein in a mutually exclusive manner with respect to the other RFGs. . . amino acid protein that is highly homologous to the amino-terminal "prepro" region of procaspoxypeptidase. The "pre" region represents a signal peptide while the "pro" region inhibits carboxypeptidase enzyme activity by binding to the active site of the enzyme before being proteolytically removed. Proteolytic cleavage of procaspoxypeptidase results in formation of mature. . .

DETD 84/03564, published on Sep. 13, 1984, and incorporated herein by reference in its entirety, may be used to screen for peptide compounds which demonstrate binding affinity for B2RP-R2 polypeptides or fragments thereof. In another embodiment, competitive drug screening assays using neutralizing antibodies specifically compete with.

DETD G protein-binding amino acid sequence DRP is found near the first transmembrane region of AAR. The extracellular portion of AAR binds to ligands that include amyloidogenic peptides. Ligand binding leads to apoptosis for the AAR-expressing cell. AAR has biological activities that comprise binding G protein components and ligands such as amyloidogenic peptides.

DETD is contacted with a cell in an amount effective to induce apoptosis of the cell. Preferred AAR ligands include amyloidogenic peptides. Further preferred AAR ligands are compounds that bind specifically to AAR and cause apoptosis in the cell expressing AAR. Further preferred AAR ligands include AAR-specific antibodies. Preferred AAR-specific.

DETD [1227] The amino-terminus of AAR is capable of binding to ligands such as amyloidogenic peptides (i.e., the beta-amyloid peptide associated with Alzheimer's disease, Amyloid Precursor Like Proteins (APLP) 1 and 2, immunoglobulin light chain, prealbumin).

DETD 84/03564, published on Sep. 13, 1984, and incorporated herein by reference in its entirety, may be used to screen for peptide compounds which demonstrate binding affinity for, or the ability to modulate, the NBHSD2, or biologically active fragments thereof in another embodiment, competitive drug screening [1597] For the purpose of the present invention, a ligand means a molecule, such as a protein, a peptide, an antibody or any synthetic chemical compound capable of binding to a GENSER protein or one of its fragments or variants or to modulate the expression of the polynucleotide coding.

DETD [1606] Alternatively, peptides, drugs or small molecules which bind to polypeptide of the present invention may be identified in competition experiments. In such assays, the GENSER protein, or a

DETD or portions thereof. Alternatively, the inhibitor can be an agent other than an antibody (e.g., small organic molecule, protein or peptide) which binds the GENSER polypeptide and blocks its activity. For example, the inhibitor can be an agent which mimics the GENSER polypeptide.

DETD Identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

=> d his

(FILE 'HOME' ENTERED AT 10:10:43 ON 19 JUN 2003)

FILE 'MEDLINE, CANCERLIT, BIOSIS, CONFSCI, EMBASE, CARLUS, USPAPFULL, PCTFULL, SCISEARCH' ENTERED AT 10:11:35 ON 19 JUN 2003

L1 151 S MORT (A) 1

L2 100 DUP REM L1 (51 DUPLICATES REMOVED)

L3 10 S L2 NOT PY=>1995

L4 4471 S FADD OR FAS (A) ASSOCIATED (A) DEATH (A) DOMAIN

L5 356 S L4 AND BIND (10A) REPTID?

L6 354 DUP REM L5 (2 DUPLICATES REMOVED)

L7 0 S L6 NOT PY=>1995

=> S 16 not PY=>1996

'1996' NOT A VALID FIELD CODE

6 FILES SEARCHED...

L8 0 L6 NOT PY=>1996

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---Logging off of STN---

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Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 10:36:11 ON 19 JUN 2003

SINCE FILE

ENTRY

73.67

TOTAL

SESSION

74.09

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:42:06 ; Search time 32 seconds
(without alignments)
1648.377 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VNAPPCRCFGGILGPIGKR.....RSGAMSPMWNDASTSEAS 256

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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9: sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	8	3.1	291	2	Q30371
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25	8	3.1	821	2	Q8VPM9	Q8VPM9 micrococcus
26	8	3.1	1109	10	Q8S750	Q8S750 oryza sativ
27	8	3.1	1209	10	Q94FG7	Q94FG7 chlamydomon
28	8	3.1	1209	10	Q9M4X9	Q9M4X9 chlamydomon
29	8	3.1	2166	5	Q9YK42	Q9YK42 drosophila
30	8	3.1	2639	5	Q76786	Q76786 antheraea p
31	8	3.1	2639	5	Q964F4	Q964F4 antheraea y
32	8	3.1	2639	5	Q964F4	Q964F4 antheraea y
33	8	3.1	2910	5	Q26008	Q26008 plasmodium
34	8	3.1	3763	5	Q8T2A1	Q8T2A1 dictyostell
35	8	3.1	48	5	Q9VN62	Q9VN62 drosophila
36	7	2.7	63	5	Q9VTH6	Q9VTH6 drosophila
37	7	2.7	77	16	Q05451	Q05451 mycobacteri
38	7	2.7	92	11	Q9CTP6	Q9CTP6 mus musculu
39	7	2.7	95	6	Q97516	Q97516 gorilla gor
40	7	2.7	95	6	Q97519	Q97519 pongo pygma
41	7	2.7	95	6	Q97520	Q97520 pongo pygma
42	7	2.7	102	17	Q8U208	Q8U208 pyrococcus
43	7	2.7	105	10	Q8S2C9	Q8S2C9 oryza sativ
44	7	2.7	106	16	Q34418	Q34418 bacillus su
45	7	2.7	111	3	Q9HGVO	Q9HGVO aspergillus

ALIGNMENTS

RESULT 1
ID Q8R2E7 PRELIMINARY: PRT: 208 AA.
AC Q8R2E7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Fas death domain associated protein.
OS FADD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=ISCHEMIC BRAIN;
RA Neame S.; (Apr-2002) to the EMBL/GenBank/DBJ databases;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=ISCHEMIC BRAIN;
RA Spadoni C.G.;
RT "Identification of neuronal caspases and involvement of death domain
RT proteins in neuronal apoptosis."
RL Theiss (2001), University of London, London, United Kingdom.
DR EMBL; AJ441127; CAD29628.1;
SQ SEQUENCE 208 AA; 23124 MW; ABA305406137CDB CRC64;

Query Match 5.9%; Score 15; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLRYVSGDLFS 95
DB 33 KRKLRYVSGDLFS 47
RESULT 2
Q9RDQ8

ID 09R08 PRELIMINARY; PRT; 295 AA.
 AC 09R08
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SC02376.
 GN SC02376 OR SCA47.04.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2)/M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbitts E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417.141-147(2002).
 DR EMBL: AL133423; CAB62708.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 295 AA; 31729 MW; FE8B3A677A451189 CRC64;

Query Match 3.5%; Score 9; DB 16; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 140
 DB 197 AGAAGAA 205

RESULT 3

ID 097518 PRELIMINARY; PRT; 99 AA.
 AC 097518;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Dopamine D4 receptor (Fragment).
 GN DRD4.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20215006; PubMed=10750051;
 RA Seaman M.I., Chang F.M., Delnard A.S., Quiñones A.T., Kidd K.R.;
 RT "Evolution of exon 1 of the dopamine D4 receptor (DRD4) gene in
 RT primates";
 RL J. Exp. Zool. 288:32-38(2000).
 DR EMBL: AF010298; AAC67226.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001.7tm.1.1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2.1.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 99 AA; 9535 MW; DACED9750184BC47 CRC64;

Query Match 3.1%; Score 8; DB 6; Length 99;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 20 AGAAGAA 27

RESULT 4

ID 09Y9X0 PRELIMINARY; PRT; 118 AA.
 AC 09Y9X0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein APE2169.
 GN APE2169.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankel A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000063; BAB81180.1; -
 KW Hypothetical protein, Complete proteome.
 SQ SEQUENCE 118 AA; 11827 MW; 68F7241C9D7678 CRC64;

Query Match 3.1%; Score 8; DB 17; Length 118;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 57 AGAAGAA 64

RESULT 5

ID 09RV6 PRELIMINARY; PRT; 224 AA.
 AC 09RV6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein DR0915.
 GN DR0915.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson J.L.,
 RA Mofatt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Yamashiro J.J., Lam P., McDonald L., Usterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioreistant bacterium Deinococcus
 RT radiodurans R1";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001944; AAP10496.1; -
 DR TIGR: DR0915;
 KW Hypothetical protein, Complete proteome.

SO SEQUENCE 224 AA; 21492 MW; DC4D770547E24AED CRC64;

Query Match 3.18; Score 8; DB 16; Length 224;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 173 AGAAGAA 180

RESULT 6

OY 09K191 PRELIMINARY; PRT; 265 AA.

AC 09K191; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OX NCBI_TaxID=1392;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=83;

RA MEDLINE=20327579; PubMed-10869077;

RA Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Kelm P.;

RT "vrb, a hypervariable open reading frame in bacillus anthracis.";

RL J. Bacteriol. 182:3989-3997(2000).

DR EMBL; AF338885; AAF6199.1;

DR HSP; P13231; HCE.

DR InterPro; IPR002395; KINNOGEN.

DR PRINTS; PR00334; KINNOGEN.

FT VARIANT 75 75 A -> T.

FT VARIANT 123 123 H -> O.

SO SEQUENCE 265 AA; 27775 MW; 8C70F8E508D28E47 CRC64;

Query Match 3.18; Score 8; DB 2; Length 265;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 244 AGAAGAA 251

RESULT 7

OY 030371 PRELIMINARY; PRT; 291 AA.

AC 030371; 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PA01;

RA MEDLINE=96254009; PubMed-8704959;

RA Stintzi A., Cornella P., Hohnadel D., Meyer J.M., Dean C., Poole K.;

RT "Novel pyoverdine biosynthesis gene(s) of Pseudomonas aeruginosa

PA01.";

RL Microbiology 142:1181-1190(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=PA01;

RX MEDLINE=99315810; PubMed-10383985;

RA Stintzi A., Johnson Z., Stonehouse M., Ochsen U., Meyer J.M.;

RA Vasil M.L., Poole K.;

RT "The pvc gene cluster of Pseudomonas aeruginosa: role in synthesis of

the pyoverdine chromophore and regulation by PtxR and pvdS.";

RL J. Bacteriol. 181:4118-4124(1999).

DR EMBL; AF002222; AAC21672.1;

SO SEQUENCE 291 AA; 33165 MW; A96B2B449132C81 CRC64;

Query Match 3.18; Score 8; DB 2; Length 291;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120

DB 224 ELASLRR 231

RESULT 8

OY 09I114 PRELIMINARY; PRT; 291 AA.

AC 09I114; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;

RA MEDLINE=20437337; PubMed-10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.;

RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.;

RA Brody R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.;

RA Smith K.A., Salter M.H., Wong G.K.-S., Wu Z., Paulsen I.T.;

RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL; AE004651; AAG05643.1;

DR Complete proteome.

SO SEQUENCE 291 AA; 33137 MW; 1D2E02B01850BD87 CRC64;

Query Match 3.18; Score 8; DB 16; Length 291;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120

DB 224 ELASLRR 231

RESULT 9

OY 09K187 PRELIMINARY; PRT; 294 AA.

AC 09K187; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OX NCBI_TaxID=1396;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 43881;

RX MEDLINE=20327579; PubMed-10869077;

RA Schnupp J.M., Krievytys A.M., Zinsner G., Price L.B., Keim P.;
 RT "vrb, a hypervariable open reading frame in bacillus anthracis."
 RL J. Bacteriol. 182:3989-3997(2000).
 DR EMBL: AF238888; AAF86203.1;
 DR InterPro: IPR002395; Kintinogen.
 DR PRINTS: PR00334; KININOGEN.
 FT NON_TER 1
 SO SEQUENCE 294 AA; 30753 MW; C05B7B37FE2E395C CRC64;

Query Match 3.1%; Score 8; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 273 AGAAGAA 280

RESULT 10

ID 09K189 PRELIMINARY; PRT; 296 AA.

AC 09K189;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Putative vrb (Fragment).
 GN VRRB.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AVCC 11778;
 RX MEDLINE=20327579; PubMed=10869077;
 RA Schnupp J.M., Krievytys A.M., Zinsner G., Price L.B., Keim P.;
 RT "vrb, a hypervariable open reading frame in bacillus anthracis."
 RL J. Bacteriol. 182:3989-3997(2000).
 DR EMBL: AF238888; AAF86201.1;
 DR InterPro: IPR002395; Kintinogen.
 DR PRINTS: PR00334; KININOGEN.
 FT NON_TER 1
 SO SEQUENCE 296 AA; 31360 MW; 332D6B6CE0A57A5A CRC64;

Query Match 3.1%; Score 8; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 273 AGAAGAA 282

RESULT 11

ID 08W0M6 PRELIMINARY; PRT; 301 AA.

AC 08W0M6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative MYB-related transcription factor.
 GN P0681B1.6 OR R1085F01.21.
 OS Oryza sativa (Rice), and
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530; 39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa niponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone:p0681B1.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa niponbare(GA3) genomic DNA, chromosome 1, BAC

clone:B1085F01." submitted (FEB-2001) to the EMBL/GenBank/DBD databases.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBD databases.
 DR EMBL: AP003022; BAB78640.1;
 DR EMBL: AP003330; BAB89885.1;
 DR InterPro: IPR001005; MYB_DNA_binding.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam: PF000249; MYB_DNA_binding; 1.
 DR Pfam: PF000988; ZF_CCHC; 1.
 DR SMART: SM00395; SANT; 1.
 DR PROSITE: PS50090; MYB_3; 1.
 SO SEQUENCE 301 AA; 31281 MW; 26B8364B7A6FB87 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 301;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 AAGAGG 141
 DB 80 AAGAGG 87

RESULT 12

ID 09V55 PRELIMINARY; PRT; 316 AA.

AC 09V55;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG6573 protein.
 GN CG6573.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Aspayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis R.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glisler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hristov D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Glabs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003525; AAF49366.1; -
 DR FlyBase; FBgn0036701; CG6573.
 SQ SEQUENCE 316 AA; 32745 MW; D99DCD8CBA14CB1 CRC64;

Query Match 3.1%; Score 8; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 AAGAAAG 141
 |||||
 DB 179 AAGAAAG 186

RESULT 13
 OYRUA8 PRELIMINARY; PRT; 316 AA.
 AC OYRUA8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein DRI483.
 GN DRI483.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Maravova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.,
 RT "Genome sequence of the radioresistant bacterium *Deinococcus*
 RT *radiodurans* RI."
 RL Science 286:1571-1577(1999).
 DR EMBL; AE001993; AAF11061.1; -
 DR TIGR; DRI483; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 316 AA; 32287 MW; C7E37F30028D53CA CRC64;

Query Match 3.1%; Score 8; DB 16; Length 316;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AAGAAAG 139
 |||||
 DB 138 AAGAAAG 145

RESULT 14
 OYRUA8 PRELIMINARY; PRT; 396 AA.
 AC OYRUA8;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 43.9 kDa protein.

GN F21E10.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eutaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Davidson S., Rohlfing T., David M., O'Brian D.,
 RT "The sequence of *A. thaliana* F21E10."
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Washu;
 RT "The *A. thaliana* Genome Sequencing Project."
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Waterston R.,
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Wilson R.,
 RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF058914; AAC13598.1; -
 DR InterPro; IPR005178; DUF300.
 DR Pfam; PF03619; DUF300; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 396 AA; 43939 MW; 61EA801F1E2C1E71 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 396;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 65
 |||||
 DB 328 SVSSSLSS 335

RESULT 15
 OYRUA8 PRELIMINARY; PRT; 400 AA.
 AC OYRUA8;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ABC transporter permease protein.
 GN FNI353.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=2186394; PubMed-1189109;
 RA Kapatal V., Anderson I., Ivanova N., Resnik G., Los T., Lykdis A.,
 RA Bhattacharya A., Bartman A., Gardner W., Greenkin G., Zhu L.,
 RA Vasielva O., Chu L., Kogan Y., Chaga O., Goldsmen E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fongstein M., Kyriades N., Overbeek R.,
 RT "Genome sequence and analysis of the oral bacterium *Fusobacterium*
 RT *nucleatum* strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE010640; AAL95549.1; -
 KW Complete proteome.
 SQ SEQUENCE 400 AA; 44260 MW; 16674867AAC35157 CRC64;

Query Match 3.1%; Score 8; DB 16; Length 400;
 Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 DTKIDSIE 178
|||||||

Db 223 DTKIDSIE 230

Search completed: June 19, 2003, 10:46:29
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:39:31; Search time 11 Seconds
(without alignments)
965,267, Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VMDPFCRCRGCGILGRLGKR.....RSGAMSPMSNDSATSEAS 256

Scoring table: OLIGO
Gapop 60.0, Capext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	68.8	208	1 FADD_HUMAN	Q13158 homo sapien
2	15	5.9	205	1 FADD_MOUSE	O61160 mus musculu
3	9	3.5	681	1 YDHE_SCHPO	G92359 schistosacch
4	8	3.1	82	1 MT21_ORYSA	P94029 oryza sativ
5	8	3.1	128	1 RL7_THREMA	P29396 thernotoga
6	8	3.1	174	1 PER_ACEME	P12347 acetabulari
7	8	3.1	258	1 YNM8_YEAST	P53862 saccharomyc
8	8	3.1	429	1 OCRA_MYCTU	Q10387 mycobacteri
9	8	3.1	468	1 IL9R_MOUSE	O01114 mus musculu
10	8	3.1	499	1 NPXR_HUMAN	O95502 homo sapien
11	8	3.1	683	1 PTNA_CORGL	Q46072 corynebacte
12	8	3.1	930	1 PRGR_RABIT	P06186 coryctolaqus
13	8	3.1	1698	1 41_DROME	G9V8R3 drosophila
14	8	3.1	1887	1 FAS2_YEAST	P19097 s fatty aci
15	7	2.7	61	1 OM06_YEAST	P33448 saccharomyc
16	7	2.7	73	1 X055_NPYAC	P14455 altograppha
17	7	2.7	121	1 RL7_CLOPE	O6XHT1 clostridium
18	7	2.7	124	1 YBF3_YEAST	P81910 saccharomyc
19	7	2.7	128	1 RL7_AOUAE	O67761 aquilex aeo
20	7	2.7	130	1 RL7_MYCTU	P37381 mycobacteri
21	7	2.7	158	1 RSD_ECOLI	P31690 escherichia
22	7	2.7	185	1 LPRB_MYCTU	Q11045 mycobacteri
23	7	2.7	193	1 HS72_CANAL	P46387 candida alb
24	7	2.7	198	1 YH13_YEAST	P38896 saccharomyc
25	7	2.7	202	1 NADD_CLOPE	O6X114 clostridium
26	7	2.7	204	1 RRA2_HUMAN	P17082 homo sapien
27	7	2.7	216	1 BENTL_XENLA	P07194 xenopus lae
28	7	2.7	219	1 YIAD_ECOLI	P37665 escherichia
29	7	2.7	245	1 HIS4_YERPE	O6ZIX3 yersinia pe
30	7	2.7	255	1 DAB2_YEAST	P511705 saccharomyc
31	7	2.7	261	1 PRP2_MOUSE	P01442 mus musculu
32	7	2.7	262	1 PENK_XENLA	P01212 xenopus lae
33	7	2.7	265	1 RL7A_FUGRU	O57592 fugu rubrip

34	7	2.7	296	1 PRP3_MOUSE	P05143 mus musculu
35	7	2.7	317	1 ISPE_ANASP	O8V561 anabena sp
36	7	2.7	327	1 PRA2_SALTI	P58716 salmonella
37	7	2.7	327	1 PRA2_SALTI	P58716 salmonella
38	7	2.7	331	1 MACS_BOVIN	P12624 bos taurus
39	7	2.7	345	1 OGGL_RAT	O70249 rattus norv
40	7	2.7	347	1 CPTP_CAEEL	P49583 caenorhabdi
41	7	2.7	361	1 HYPB_ALICE	P31902 alcaligenes
42	7	2.7	367	1 PROB_MYCLE	O9CB25 mycobacteri
43	7	2.7	373	1 YL02_PICAN	P34735 picula angu
44	7	2.7	376	1 PROB_MYCTU	P71910 mycobacteri
45	7	2.7	378	1 DNJ2_MYCLE	Q49762 mycobacteri

ALIGNMENTS

RESULT 1	ID	FADD_HUMAN	STANDARD:	PRT:	208 AA.
AC	Q13158	Q14866			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	FADD protein (FAS-associating death domain-containing protein)				
DE	(Mediator of receptor induced toxicity).				
GN	FADD OR MORT1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.				
RC	TISSUE-Umbilical vein endothelial cells;				
RX	MEDLINE-95277837; PubMed-7538907;				
RA	Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;				
RT	"FADD, a novel death domain-containing protein, interacts with the				
RT	death domain of Fas and initiates apoptosis.";				
RL	Cell 81:505-512(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-95229578; PubMed-7536190;				
RA	Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,				
RT	Wallach D.;				
RL	"A novel protein that interacts with the death domain of Fas/APo1				
RL	contains a sequence motif related to the death domain.";				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Lung;				
RA	Strauberg R.;				
RT	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	STRUCTURE BY NMR OF 1-83.				
RX	MEDLINE-96241233; PubMed-9582077;				
RA	Ederstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,				
RT	Lenardo M.J., Fesik S.W.;				
RL	"NMR structure and mutagenesis of the FADD (Mort1) death-effector				
RL	domain.";				
CC	Nature 392:941-945(1998).				
CC	-I- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR				
CC	CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNF-R1 RECEPTORS. THE				
CC	RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX				
CC	(DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8				
CC	INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC				
CC	CSTEINE PROTEASES) MEDIATING APOPTOSIS.				
CC	-I- SUBUNIT: INTERACTS WITH CEIAR.				
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT				
CC	FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.				
CC	-I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE				
CC	CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.				
CC	-I- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).				
CC	-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				

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CC or send an email to license@isb-sib.ch).
DR EMBL: U24231; AAA6517.1; -
DR EMBL: X84709; CA559197.1; -
DR EMBL: BC000334; AAH0034.1; -
DR PDB: 1A1W; 16-FEB-99.
DR PDB: 1A1Z; 16-FEB-99.
DR Genew; HGNC:3573; FADD.
DR MIM; 602457; -
DR InterPro: IPR001875; DED.
DR InterPro: IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00031; DED; 1.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS50168; DED; 1.
DR Apoptosis; 3D-structure.
DR DOMAIN; 3 81 DED.
FT DOMAIN 97 181 DEATH.
FT MUTAGEN 121 121 V->N: NO INTERACTION WITH FAS RECEPTOR.
FT CONFLICT 32 32 G->V (IN REF. 2)
SQ SEQUENCE 208 AA; 23279 MW; 0E65E2852E83507 CRC64;

Query Match 68.8%; Score 176; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 7.8e-164;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLVVOGSLDFFSLRQNDLEPGHTELRRLASLRHDLRLRYDPEAAGAAAP 140
DB 33 KRRLVVOGSLDFFSLRQNDLEPGHTELRRLASLRHDLRLRYDPEAAGAAAP 92
QY 141 GEEDLCAAFNVICDNGKMRRLARQLKYSDETKIDSIEDRYPNLTERVRESLRINTE 200
DB 93 GEEDLCAAFNVICDNGKMRRLARQLKYSDETKIDSIEDRYPNLTERVRESLRINTE 152
QY 201 KENATVAHLVGLRSCQANLVADLVQEQARLQNRSGAMSPWNSDASTSEAS 256
DB 153 KENATVAHLVGLRSCQANLVADLVQEQARLQNRSGAMSPWNSDASTSEAS 208

RESULT 2
FADD_MOUSE STANDARD; PRT; 205 AA.
ID FADD_MOUSE
AC 061160; 061082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (FAS-associated death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MORT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96220459; PubMed=8649383;
RA Zhang J., Winoto A.;
RT "A mouse Fas-associated protein with homology to the human MORT1/FADD
RL protein is essential for Fas-induced apoptosis."
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96152659; PubMed=85565075;
RA Hsu H., Shu H.-B., Fan M.G., Goeddel D.V.;

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RT "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
RT receptor 1 signal transduction pathways."
RL Cell 84:299-308(1996).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U50406; AAB07789.1; -
DR EMBL: U43184; AAA97876.1; -
DR HSSP; Q13158; 1A1Z.
DR MGD; MGI:109324; Fadd.
DR InterPro: IPR001875; DED.
DR InterPro: IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00031; DED; 1.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS50168; DED; 1.
DR Apoptosis.
DR DOMAIN; 3 81 DED.
FT DOMAIN 97 181 DEATH.
FT CONFLICT 168 168 C->F (IN REF. 2).
SQ SEQUENCE 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;

Query Match 5.9%; Score 15; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LRRELLASLRHDL 124
DB 62 LRRELLASLRHDL 76

RESULT 3
YDHE_SCHPO STANDARD; PRT; 681 AA.
ID YDHE_SCHPO
AC 092359;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C69.14 in chromosome 1.
GN SPAC69.14.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

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RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowich E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Stmonds M., Squares R., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodard J., Volckert G., Aert R., Robben J., Grymptiez B.,
 RA Willems I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehner H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wandt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerretti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Siparovsky G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schistosoma mansoni* pombe.";
 RL Nature 415:871-880(2002)
 CC -1- SIMILARITY: BELONGS TO THE PUMILIO/MPIS FAMILY.
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 DR EMBL: Z81317; CAB03616.1; -
 DR InterPro: IPR001313; Pumilio/Puf.
 DR Pfam: PF00806; PUF; 8.
 DR SMART: SM00025; Pumilio; 8.
 KM Hypothetical protein.
 SQ SEQUENCE 681 AA; 73292 MW; 755A25C68A92D727 CRC64;
 QY 58 SVSSSSSS 66
 DB 329 SVSSSSSS 337
 Query Match 3.5%; Score 9; DB 1; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 4
 MT21.ORYSA STANDARD; PRT; 82 AA.
 AC P94029;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein-like protein type 2.
 GN MT-2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubacteriodes; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. Tainong 67; TISSUE-Root;
 RX MEDLINE-97134941; PubMed-8980501;
 RA Hsieh H.M., Liu W.K., Chang A., Huang P.C.;
 RT "RNA expression patterns of a type 2 metallothionein-like gene from
 rice.";
 RL Plant Mol. Biol. 32:525-529(1996).
 CC -1- FUNCTION: METALLOTHIONEIN HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
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 DR EMBL: U43530; AAC49627.1; -
 DR EMBL: D89931; BAA1038.1; -
 DR InterPro: IPR000347; Metallothion_15.
 DR Pfam: PF01439; Metallothio_2; 1.
 DR ProDom: PD001611; Metallothion_15; 1.
 KM Metal-binding; Metal-thiolate cluster; Multigene family.
 SQ SEQUENCE 82 AA; 7852 MW; 8DC0628B65503C4 CRC64;
 QY 131 EAGAAAGA 138
 DB 54 EAGAAAGA 61
 Query Match 3.1%; Score 8; DB 1; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1; 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 5
 RL7.THEMA STANDARD; PRT; 128 AA.
 AC P29396;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L7/L12.
 GN RPL7 OR TM0457.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RX MEDLINE-94232816; PubMed-8177738;
 RA Palm P., Schleper C., Arnold-Ammer I., Holz I., Meier T.,
 RA Lottspeich F., Zillig W.;
 RT "The DNA-dependent RNA-polymerase of *Thermotoga maritima*;
 RT characterisation of the enzyme and the DNA-sequence of the genes for
 RT the large subunits.";
 RL Nucleic Acids Res. 21:4904-4908(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RX MEDLINE-94232816; PubMed-8177738;
 RA Palm P., Schleper C., Arnold-Ammer I., Holz I., Meier T.,
 RA Lottspeich F., Zillig W.;
 RT "The DNA-dependent RNA-polymerase of *Thermotoga maritima*;
 RT characterisation of the enzyme and the DNA-sequence of the genes for
 RT the large subunits.";
 RL Nucleic Acids Res. 21:4904-4908(1993).
 RN [3]
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 RN [48]
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 RN [51]
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 RX MEDLINE-94232816; PubMed-8177738;
 RA Palm P., Schleper C., Arnold

OY	60 SSSLSSE 67
Db	41 SSSLSSE 48

RESULT 7

ID	YNM8_YEAST	STANDARD:	PRT:	258 AA.
AC	PS38652:			
Dt	01-OCT-1996 (Rel. 34, Created)			
Dt	01-OCT-1996 (Rel. 34, Last sequence update)			
Dt	01-OCT-1996 (Rel. 34, Last annotation update)			
De	Hypothetical 28.6 kDa protein in URE2-SSU72.intergenic region precursor.			
DE	YNL228W OR N1249.			
GS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OX	Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
XX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97051596; PubMed-8896273;			
RA	Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;			
RT	"The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading frames including a novel gene encoding a globin-like domain."			
RL	Yeast 12:1071-1076(1996).			
RN	[2]			
RP	SEQUENCE OF 71-258 FROM N.A.			
RA	Duesterhoef A., Floeth M., Flitz C., Heuss-Netzel D., Hilbert H., Moschl D.			
CC	(MAR-1996) to the EMBL/GenBank/DBJ databases.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein (potential).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sdb.ch/announce/ or send an email to license@isb-sdb.ch).			
CC	-----			
DR	EMBL; 269381; CA93370.1; -			
DR	EMBL; 271504; CA96131.1; -			
DR	SGD, S0005172; YNL228W			
KM	Hypothetical protein; Signal; Transmembrane.			
FT	SIGNAL 1 23 POTENTIAL.			
FT	CHAIN 24 258. HYPOHETICAL PROTEIN YNL228W.			
FT	TRANSMEM 65 85 POTENTIAL.			
FT	TRANSMEM 124 144 POTENTIAL.			
FT	TRANSMEM 231 251 POTENTIAL.			
FT	DOMAIN 79 82 POLY-PHE.			
FT	DOMAIN 88 92 POLY-SER.			
FT	DOMAIN 129 141 N-LINKED (GICNAC. . .) (POTENTIAL).			
FT	CAROHWD 118 118 N-LINKED (GICNAC. . .) (POTENTIAL).			
FT	CAROHWD 206 206 N-LINKED (GICNAC. . .) (POTENTIAL).			
SEQ	SEQUENCE 258 AA; 28641 MW; 24F58C70CD10E86C CRC64;			

Query Match 3.1%; Score 8; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	60 SSSLSSE 67
Db	165 SSSLSSE 172

RESULT 8

ID	OCRA_MYCTU	STANDARD:	PRT:	429 AA.
AC	Q10387:			
Dt	01-OCT-1996 (Rel. 34, Created)			
Dt	01-OCT-1996 (Rel. 34, Last sequence update)			

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiqinol-cytochrome C reductase iron-sulfur subunit (Rieske iron-
 sulfur protein).
 GN OCRA OR RV2195 OR MT2251 OR MTCV190.06.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinobacteridae;
 OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=9825967; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnter T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornby T., Jaffe K., Krogan N., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.,
 RT Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh.
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Ormazabal L.A., Esmailova M.D., Salzberg S.L.,
 RA Bacher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.,
 RT Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX. THE RIESKE PROTEIN IS A HIGH POTENTIAL 2FE-2S PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNIT OF THE UBIQUINOL-CYTOCHROME C COMPLEX
 CC ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A CYTOCHROME C SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: TO RIESKE PROTEINS FROM OTHER SOURCES (MITOCHONDRIA,
 CC BACTERIAL, CHLOROPLAST).
 CC -----
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 CC -----
 DR EMBL: Z70283; CA94264.1;
 DR EMBL: AE007071; AA46537.1;
 DR TIGR: MT2251;
 DR Tuberculast: RV2195;
 DR InterPro: IPR001281; Rieske.
 DR Pfam: PF00355; Rieske; 1.
 DR PROSITE: PS00199; RIESKE_1; FALSE_NEG;
 DR PROSITE: PS00200; RIESKE_2; 1.
 KW Electron transport; Iron-sulfur; Oxidoreductase; Transmembrane;
 KM Complete proteome.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 137 157 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT METAL 353 355 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 355 355 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 372 372 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 375 375 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 375 375 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT DISULFID 358 374 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 46922 MW; C22C87EC283FE0EE CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 LGHYVRK 83
 Db 329 LGHYVRK 336
 RESULT 9
 ID IL9R_MOUSE STANDARD; PRT; 468 AA.
 AC 001114;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Interleukin-9 receptor precursor (IL-9R).
 GN IL9R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=92302307; PubMed=1376929;
 RA Renaldi J.C., Druet C., Kermouni A., Housiau F., Dyttenhove C.,
 RA van Roost E., van Snick J.,
 RT "Expression cloning of the murine and human interleukin 9 receptor
 RT cDNAs."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M84746; AA37871.1;
 DR PIR: A45268; A45268.
 DR M84746; M84746; 119.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003531; Hemopoietin_S_F1.
 DR PROSITE: PS01355; HEMATOPOIETIN_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; T-cell.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 468 INTERLEUKIN-9 RECEPTOR.
 FT DOMAIN 38 270 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 271 291 POTENTIAL.
 FT DOMAIN 292 468 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 149 242 FIBRONECTIN TYPE-III.
 FT CARBOHYD 116 116 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 468 AA; 52260 MW; BBE7179FD72E29A5 CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 33 GARRAGPQ 40
 Db 328 GARRAGPQ 335
 RESULT 10
 ID NPXR_HUMAN STANDARD; PRT; 499 AA.
 AC 095502;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DR HSSP: P08837; 1GIC.
 DR InterPro: IPR001137; PTS_EI1A.
 DR InterPro: IPR001996; PTS_EI1B.
 DR InterPro: IPR003352; PTS_EI1C.
 DR Pfam: PF00358; PTS_EI1A.1.
 DR Pfam: PF00367; PTS_EI1B.1.
 DR Pfam: PF02378; PTS_EI1C.1.
 DR ProDom: PD001476; PTS_EI1B.1.
 DR ProDom: PD002483; PTS_EI1A.1.
 DR TIGRfams: TIGR00830; PTBA.1.
 DR PROSITE: PS00371; PTS_EI1A.1.
 DR PROSITE: PS01035; PTS_EI1B_CYS.1.
 DR Phosphotransferase system; Sugar transport; Transferase;
 KM Phosphorylation; Transmembrane
 FT DOMAIN 1 43 EI1B DOMAIN
 FT DOMAIN 1 43 EI1C DOMAIN
 FT DOMAIN 1 43 EI1A DOMAIN
 FT TRANSMEM 126 683 POTENTIAL
 FT TRANSMEM 126 146 POTENTIAL
 FT TRANSMEM 162 182 POTENTIAL
 FT TRANSMEM 193 213 POTENTIAL
 FT TRANSMEM 226 246 POTENTIAL
 FT TRANSMEM 260 280 POTENTIAL
 FT TRANSMEM 303 323 POTENTIAL
 FT TRANSMEM 344 364 POTENTIAL
 FT TRANSMEM 376 396 POTENTIAL
 FT TRANSMEM 409 429 POTENTIAL
 FT TRANSMEM 442 462 POTENTIAL
 FT MOD_RES 28 28 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 602 602 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 683 AA; 72571 MW; 0B42CAEC60828075 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 683;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 |||||
 Db 510 AGAAGAA 517

RESULT 12
 PRGR_RABIT STANDARD; PRT; 930 AA.
 AC P06186;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Progesterone receptor (PR).
 GN PGR OR NR3C3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067449; PubMed=3538016;
 RA Loosfelt H., Atter M., Mistrall M., Guichon-Mantel A., Meriel C.,
 RA Logeat F., Benarous R., Milgrom E.;
 RT Cloning and sequence analysis of rabbit progesterone-receptor
 RT complementary DNA.
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC -1- THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC MN3 SUBFAMILY.
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DR EMBL: M14547; AAA31443.1;
 DR PIR: A25923; A25923.
 DR HSSP: P06401; 1A28.
 DR TRANSFAC: T00697;
 DR InterPro: IPR000536; Hormone_rec_119.
 DR InterPro: IPR000128; Progesterone_receptor.
 DR InterPro: IPR001628; ZnF_C4steroid.
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; zf-C4.1.
 DR Pfam: PF02161; Prog_receptor.1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; ZnF_C4steroid.1.
 DR SMART: SM00430; HOL1.1.
 DR SMART: SM00399; ZnF_C4.1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR.1.
 KM Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 FT Zinc-finger; Steroid-binding.
 FT DOMAIN 1 565 MODULATING, PRO-RICH
 FT DNA_BIND 568 633 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 568 588 C4-TYPE.
 FT ZN_FING 604 628 C4-TYPE.
 FT DOMAIN 678 930 STEROID-BINDING.
 FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 930 AA; 98666 MW; 644FF4C13BF883 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 930;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 GAAAGAP 140
 |||||
 Db 503 GAAAGAP 510

RESULT 13
 ID 41_DROME STANDARD; PRT; 1698 AA.
 AC Q9V8R9; Q24440; Q24441; Q24442; Q9V8R8; Q9V8S0.
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein 4.1 homolog (Coracle protein).
 GN CORA OR CGI1949.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), AND FUNCTION.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=94215495; PubMed=8162854;
 RA Felton R.G., Dawson I.A., Artavanis-Tsakonas S.;
 RA "A Drosophila homologue of membrane-skeleton protein 4.1 is associated
 RA with septate junctions and is encoded by the coracle gene."
 RL Development 120:545-557(1994).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4).
 CC STRAIN=Berkley;
 CC MEDLINE=20196006; PubMed=10731132;
 CC Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC Sutton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,
 CC Brandon R.C., Rogers Y.-H.C., Blazek R.G., Change M., Pfeiffer B.D.,
 CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKiss G.L.G.,
 CC Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 CC Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Beeson P.V., Bernman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Bussey D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport U.B., Davies P.,
RA de Palacios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gebriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Honck J.,
RA Hostin D., Houston K.A., Howland T.J., Mel M.-H., Ibbegam C.,
RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lal X.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Nobarary C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paelel J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Slden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Wotley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gldbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195(2000).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 5).
RP STRAIN-Berkeley;
RC Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnak D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paelel J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Gelniker S.,
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: An integral component of the septate junction. May play
CC a role in cell-cell interactions that are necessary for proper
CC development. Vital for embryonic development.
CC -1- SUBCELLULAR LOCATION: Septate junction in the apical-lateral
CC domain of epithelial cells during embryonic and imaginal disk
CC development.
CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; 1 (shown here), 2, 3, 4 and 5;
CC may be produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: At onset of germ band retraction, expression
CC is seen in epidermis, hindgut and foregut. During retraction,
CC expression extends to tracheal branches and salivary glands.
CC -1- DEVELOPMENTAL STAGE: Expressed weakly in 4-8 hour embryos, more
CC abundant expression in 8-12 hours and remains throughout later
CC embryonic and larval stages.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL, L27467, AAB59187.1, -
DR EMBL, L27468, AAA28742.1, -
DR EMBL, L27469, AAA28743.1, -
DR EMBL, AE003796, AAF57591.1, -
DR EMBL, AE003796, AAF57592.1, -
DR EMBL, AE003796, AAF57593.1, -
DR EMBL, AY070992, AAL46614.1, -
DR FlyBase, FBgn010436, core,
DR InterPro, IPR000299, Band_4.1.

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.N.,
 RA Dietrich F.S., Dilius H., Dipaolo T., Dubois E., Duesterhoeft A.,
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 RA Hall J., Hobling U., Heumann K., Hilbert H., Hillier L.,
 RA Hunkeler-Smith S., Hyman R., Johnston M., Kaiman S., Klatte K.,
 RA Komp C., Kuri O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
 RA Marathe R., Messing F., Mewes H.-W., Mittipati S., Moestl D.,
 RA Mueller-Auer S., Namath A., Newtich U., Oeffner P., Pearson D.,
 RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scherf M.,
 RA Scherens B., Schramm S., Schroeder M., Sidcu A.M., Tettelin H.,
 RA Urrutazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
 RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
 RA Zhong W.W., Zollner A., Vo D.H., Hani J.,
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.",
 RT Nature 387:103-105(1997).
 RL (4)
 RN NOTAGENESIS OF GLY-1250.
 RP STRAIN-S288c;
 RX MEDLINE-94316198; PubMed-8041367;
 RA Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
 RA Omura S.;
 RT "Cerulenin-resistant mutants of Saccharomyces cerevisiae with an
 altered fatty acid synthase gene";
 RT Mol. Gen. Genet. 244:90-96(1994).
 CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
 LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-
 CC CARRIER PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH -> a
 CC long-chain fatty acid + (N+1) COA + N CO(2) + 2N NADP(+).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] -> 3-oxoacyl-[acyl-carrier protein] + CO(2) +
 CC [acyl-carrier protein]
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: [alpha(6)beta(6)] hexamers of two multifunctional
 CC subunits (alpha and beta).
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
 CC OTHER FUNGI.
 CC
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 DR EMBL: J03936; AAA34601.1; -
 DR EMBL: X76890; CA54218.1; -
 DR EMBL: X94561; CA64236.1; -
 DR EMBL: Z73586; CA97947.1; -
 DR EMBL: Z73587; CA97948.1; -
 DR PIR: A31107; A31107; -
 DR SGD: S0006152; FAS2;
 DR InterPro: IPR002582; ACPS;
 DR InterPro: IPR00794; ketoacyl-synt.
 DR InterPro: IPR004568; Pantethn_ttn.
 DR InterPro: IPR003880; Pantethn_attach.
 DR Pfam: PF00109; ketoacyl-synt; 1.
 DR Pfam: PF01648; ACPS; 1.
 DR Pfam: PF02801; ketoacyl-synt_C; 1.
 DR ProDom: PD004282; ACPS; 1.
 DR TIGRFAMs: TIGR00556; pantethn_ttn; 1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; 1.
 DR PROSITE: PS00606; B_KETOACYL-SYNTHASE; 1.
 KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
 KM Transferase; NADP; Phosphopantetheine;
 FT DOMAIN 1 ? ACT1 CARRIER (ACP).
 FT 675 874 BETA-KETOACYL REDUCTASE.
 FT DOMAIN 1149 1363 BETA-KETOACYL SYNTHASE.

FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).
 FT ACT_SITE 1305 1305 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT MOTAGEN 1250 1250 G->S: CERULENIN-RESISTANCE.
 FT CONFLICT 310 310 G -> I (IN REF. 1).
 FT CONFLICT 594 594 T -> T (IN REF. 1).
 FT CONFLICT 941 1019 AKRKEIVETSEVRKAVSITALEHKVNGNSADAAAYOE
 FT IORPANIQDPEPLPYKQYQIAPAPEGLDLERYI ->
 FT CLNCVSKMLKLEKROFPEKSLMSITSLVAILMLMMS
 FT KFNQELTFNWTSONRHNNTNLKPLSLKVCWIMWELF
 FT (IN REF. 1).
 FT KRWMEA -> KWNGS (IN REF. 1).
 FT A -> S (IN REF. 1).
 FT N -> T (IN REF. 1).
 FT CONFLICT 1408 1408
 FT CONFLICT 1671 1671
 FT CONFLICT 1887 AA; 206946 MW; 08B872734CF3AEEA CRC64;
 SQ SEQUENCE
 Query Match 3.18; Score 8; DB 1; Length 1887;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;
 Db 132 AGAAGAA 139
 11111111
 314 AGAAGAA 321
 RESULT 15
 OM06_YEAST STANDARD; PRT; 61 AA.
 AC P33448;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitochondrial import receptor subunit TOM6 (Mitochondrial import-site
 DE protein ISp6) (Translocase of outer membrane 6 kDa subunit).
 DE TOM6 OR ISp6 OR YOR045W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID:4932;
 RN [1]
 RP MEDLINE-9345447; PubMed-8344244;
 RX Kassenbrock C.K., Cao W., Douglas M.G.;
 RA "Genetic and biochemical characterization of ISp6, a small
 RT mitochondrial outer membrane protein associated with the protein
 RT translocation complex";
 RL EMBO J. 12:3023-3034(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SEEMS TO ACT AS A MODULATOR OF THE DYNAMICS OF THE
 CC MITOCHONDRIAL PROTEIN TRANSPORT MACHINERY. SEEMS TO PROMOTE THE
 CC ASSOCIATION OF SUBUNITS OF THE OUTER MEMBRANE TRANSLOCASE.
 CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
 CC LEAST 8 DIFFERENT PROTEINS (TOM5, TOM6, TOM7, TOM20, TOM22,
 CC TOM37, TOM40 AND TOM70).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC outer membrane.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC
 DR EMBL: Z22815; CA80469.1; -
 DR EMBL: Z74953; CA99236.1; -
 DR PIR: S35320; S35320.
 DR SGD: S0005571; TOM6.
 DR Transport; Protein transport; Outer membrane; Mitochondrion;
 KW Transmembrane.

FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 32 52 POTENTIAL.
 FT DOMAIN 53 61 MITOCHONDRIAL (POTENTIAL).
 SQ SEQUENCE 61 AA; 6407 MW; EE3F295BC0FE7240 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 61;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 GAAAGAA 139
 |||||
 Db 9 GAAAGAA 15

Search completed: June 19, 2003, 10:45:50
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:44:01 ; Search time 40 Seconds
(Without alignments)
615.260 Million cell updates/sec

Title: US-09-933-814-2

Sequence: 1 VNGAPRCRFGCGILGPKR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	176	68.8	208	A56912	FADD protein - hum
2	9	3.5	681	T39076	serine rich pumili
3	8	3.1	82	T03727	metallothionein-11
4	8	3.1	118	D72524	hypothetical prote
5	8	3.1	128	R7HG12	ribosomal protein
6	8	3.1	174	S00273	period clock prote
7	8	3.1	224	B75460	hypothetical prote
8	8	3.1	238	S63194	probable membrane
9	8	3.1	291	A83364	proveridine biosynt
10	8	3.1	316	G75388	hypothetical prote
11	8	3.1	396	T01201	hypothetical prote
12	8	3.1	429	D70784	probable Rieseke [2
13	8	3.1	467	I56896	gene gfi-2 protein
14	8	3.1	468	A45268	interleukin-9 rece
15	8	3.1	639	G86455	hypothetical prote
16	8	3.1	930	A25923	progesterone recep
17	8	3.1	1698	T13800	coracle gene prote
18	8	3.1	1887	S61703	fatty-acid synthas
19	8	3.1	2639	T31328	fibroin - Chinese
20	8	3.1	2910	T28156	DNA-directed RNA p
21	7	2.7	61	S35320	ISBP protein - yea
22	7	2.7	73	H72856	Acorf-55 protein -
23	7	2.7	77	F70598	probable PE protei
24	7	2.7	106	D69808	hypothetical prote
25	7	2.7	113	A75626	salicylate monooxy
26	7	2.7	124	S45788	probable membrane
27	7	2.7	128	E70466	ribosomal protein
28	7	2.7	128	T30714	hypothetical prote
29	7	2.7	130	A70615	probable ribosomal

30	7	2.7	130	S41123	ribosomal protein
31	7	2.7	135	AH2100	hypothetical prote
32	7	2.7	135	A42098	transcription fact
33	7	2.7	141	T34419	hypothetical prote
34	7	2.7	150	A59103	hypothetical prote
35	7	2.7	158	F65206	probable transcript
36	7	2.7	158	F91243	probable transcript
37	7	2.7	158	D86091	serine-rich protei
38	7	2.7	163	T17700	hypothetical prote
39	7	2.7	183	S67784	probable IPRB prote
40	7	2.7	185	B70755	probable IPRB prote
41	7	2.7	188	D29149	proline-rich prote
42	7	2.7	190	A83298	regulatory factor
43	7	2.7	192	S70267	outer surface prot
44	7	2.7	194	F83219	hypothetical prote
45	7	2.7	194	F91169	hypothetical prote

ALIGNMENTS

RESULT 1
A56912
FADD protein - human
N:Alternate names: FAS-associating death domain containing protein FADD; mediator of
C:Species: Homo sapiens (man)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 01-Dec-2000
C:Accession: A56912; I38041
R:Chinnaiyan, A.M.; O'Rourke, R.; Tewari, M.; Dixit, V.M.
Cell 81, 505-512 (1995)
A>Title: FADD, a novel death domain-containing protein, interacts with the death doma
A:Reference number: A56912; MUID:95277837; PMID:7538907
A:Accession: A56912
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <CHI>
A:Cross-references: GB:U24231; NID:9809486; PIDN:AA86517.1; PID:9809487
R:Boldin, M.P.; Varfolomeev, E.E.; Pancier, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D.
J. Biol. Chem. 270, 7795-7798 (1995)
A>Title: A novel protein that interacts with the death domain of Fas/APo1 contains a
A:Reference number: I38041; MUID:95229578; PMID:7536190
A:Accession: I38041
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-31, 'V', 33-208 <RES>
A:Cross-references: EMBL:X84709; NID:9791037; PIDN:CA59197.1; PID:9791038
C:Genetics:
A:Gene: GDB:FADD; MORT1
A:Cross-references: GDB:1320394
C:Superfamily: receptor-induced toxicity mediator MORT1
C:Keywords: apoptosis

Query Match 68.8%; Score 176; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1,4e-162;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLERYVSGDLSFMLEQNDLEPGHTELLRELLASLRRLDLRRVDDFEAGAAAGAP 140
DB 33 KRKLERYVSGDLSFMLEQNDLEPGHTELLRELLASLRRLDLRRVDDFEAGAAAGAP 92
QY 141 GEEDLCAAFNYICNVGKDRRLAROLKVSPTKIDSIDRYPRLUTEKVESLAIWKTE 200
DB 93 GEEDLCAAFNYICNVGKDRRLAROLKVSPTKIDSIDRYPRLUTEKVESLAIWKTE 152
QY 201 KENATVAHLVGLALSCQNTLVADLVQEVQARDLQNSGASPMNSDASTSEAS 256
DB 153 KENATVAHLVGLALSCQNTLVADLVQEVQARDLQNSGASPMNSDASTSEAS 208

RESULT 2
T39076
serine rich pumilio family rna binding domain pr otein - fission yeast (Schizosacchar
C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39076
 R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, V.
 Submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21825
 A:Accession: T39076
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-681 <NCR>
 A:Cross-references: EMBL:281317; PIDN:CA03616.1; GSPDB:GN00066; SPDB:SPAC669.14
 A:Experimental source: strain 972h-; cosmid c669
 C:Genetics:
 A:Gene: SPDB:SPAC669.14
 A:Map position: 1
 A:Introns: 580/3

Query Match
 Best Local Similarity 100.0%; Score 9; DB 2; Length 681;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 66
 Db 329 SVSSSLSS 337

RESULT 3
 T03727
 metallothionein-like protein - rice
 C:Species: Oryza sativa (rice)
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
 C:Accession: T03727
 R:Chen, W.M.; Hsieh, H.M.; Huang, P.C.
 submitted to the EMBL Data Library, December 1996
 A:Description: Signification of two introns in type 2 rice metallothionein-like gene.
 A:Reference number: Z15032
 A:Accession: T03727
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <CHD>
 A:Cross-references: EMBL:DB9931; PIDN:BA14038.1
 A:Experimental source: cv. Tainung 67, root
 C:Genetics:
 A:Gene: rgmt-2
 A:Introns: 22/2; 48/2
 C:Superfamily: metallothionein

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 82;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 EAGAAAGA 138
 Db 54 EAGAAAGA 61

RESULT 4
 D72524
 hypothetical protein APE2169 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: D72524
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahara, H.; Takamizawa, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MID:99310339; PMID:10382966
 A:Accession: D72524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BA81180.1; PID:41044966; PID:9510
 A:Experimental source: strain K1
 C:Genetics:

A:Gene: APE2169

Query Match
 Best Local Similarity 100.0%; Score 8; DB 2; Length 118;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 Db 57 AGAAGAA 64

RESULT 5
 R7HG12
 ribosomal protein L7/L12 - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 21-Jul-2000
 C:Accession: E44466; S41465; B72376; S19902
 R:Li, D.; Dennis, P.P.
 J. Biol. Chem. 267, 22787-22797, 1992
 A:Title: The organization and expression of essential transcription translation comp
 A:Reference number: A44466; MID:93054590; PMID:1429627
 A:Accession: E44466
 A:Molecule type: DNA
 A:Residues: 1-128 <LIA>
 A:Cross-references: EMBL:Z11839; NID:9407020; PIDN:CA47862.1; PID:948187
 A:Note: sequence extracted from NCBI backbone (NCBI:118058)
 R:Palin, P.; Schleper, C.; Arnold-Hummer, I.; Holz, I.; Meyer, T.; Lottspeich, F.; Zil
 Nucleic Acids Res. 21, 4904-4908, 1993
 A:Title: The DNA-dependent RNA-polymerase of Thermotoga maritima; characterisation o
 A:Reference number: S41465; MID:94232816; PMID:8177738
 A:Accession: S41465
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 C:M.
 A:Molecule type: DNA
 A:Residues: 1-128 <PAL>
 A:Cross-references: EMBL:X72695; NID:9425255; PIDN:CA51245.1; PID:9425257
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hl
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MID:99287316; PMID:10360571
 A:Accession: B72376
 A:Molecule type: DNA
 A:Residues: 1-128 <ARN>
 A:Cross-references: GB:AE001723; GB:AE000512; NID:94980953; PIDN:AA035540.1; PID:949
 A:Experimental source: strain MS8
 C:Genetics:
 A:Gene: TM0457
 C:Superfamily: Escherichia coli ribosomal protein L12
 C:Keywords: protein biosynthesis; ribosome

Query Match
 Best Local Similarity 100.0%; Score 8; DB 1; Length 128;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 Db 45 AGAAGAA 52

RESULT 6
 S00273
 period clock protein - Acetabularia mediterranea chloroplast (fragment)
 C:Species: chloroplast Acetabularia mediterranea
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000
 C:Accession: S00273
 R:Li-Weber, M.; de Groot, E.J.; Schweiger, H.G.
 Mol. Gen. Genet. 209, 1-7, 1987
 A:Title: Sequence homology to the Drosophila per locus in higher plant nuclear DNA a
 A:Reference number: S00273
 A:Accession: S00273
 A:Molecule type: DNA

A:Residues: 1-174 <LIV>
 A:Cross-references: EMBL:X05806; NID:g11316; PIDN:CA29249.1; PID:g1334349
 C:Genetics:
 A:Genome: chloroplast
 C:Superfamily: period clock protein; EGF homology
 C:Keywords: chloroplast; circadian rhythm
 F:49-138/Region: 2-residue repeats (G-T)

Query Match 3.1%; Score 8; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 SSSLSSE 67
 DB 41 SSSLSSE 48

RESULT 7
 B75460
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75460
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 Science 266, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75460
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <MHI>
 A:Cross-references: GB:AE001944; GB:AE000513; NID:g6458634; PIDN:AA10496.1; PID:g645864
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0915
 A:Map position: 1

Query Match 3.1%; Score 8; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139
 DB 173 AGAAGAA 180

RESULT 8
 S63194
 Probable membrane protein YNL228w - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N1249
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
 C:Accession: S63194; S63186; S67370; S72088
 R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63188
 A:Accession: S63194
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z71504; NID:g1302248; PID:g239626; PID:g1302249; MIPS:YNL228w
 A:Experimental source: strain S288C
 R:Duesterhoeft, A.; Floeth, M.; Fritze, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62944
 A:Accession: S63186
 A:Molecule type: DNA
 A:Residues: 71-258 <DUE>
 A:Cross-references: EMBL:Z71504; MIPS:YNL228w
 A:Experimental source: strain S288C
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the EMBL Data Library, February 1996

A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.
 A:Reference number: S67355
 A:Accession: S67370
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PID:e221816; PID:g1183986
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 Yeast 12, 1071-1076, 1996
 A:Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading
 A:Reference number: S72073; MUID:97051596; PMID:8896273
 A:Accession: S72088
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-258 <PAV>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CA93370.1; PID:g1183986
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Cross-references: SGD:S0005172
 A:Map position: 14L
 A:Note: YNL228w
 C:Keywords: transmembrane protein
 F:723/Domain: transmembrane #status predicted <TM1>
 F:65-81/Domain: transmembrane #status predicted <TM2>
 F:129-145/Domain: transmembrane #status predicted <TM3>
 F:230-246/Domain: transmembrane #status predicted <TM4>

Query Match 3.1%; Score 8; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 SSSLSSE 67
 DB 165 SSSLSSE 172

RESULT 9
 A83364
 pyoverdine biosynthesis protein PycB PA2255 [Imported] - *Pseudomonas aeruginosa* (stra
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: A83364
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: A83364
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <STO>
 A:Cross-references: GB:AE004651; GB:AE004091; NID:g9948277; PIDN:AA05643.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: pycB; PA2255

Query Match 3.1%; Score 8; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRR 120
 DB 224 ELASLRR 231

RESULT 10
 G75388
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75388
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; PMID:10567266

A:Accession: G75388

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1316 <NR1>

A:Cross-references: GB:AE001993; GB:AE000513; NID:96459244; PIDN:AAE11061.1; PID:9645925

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1483

A:Map position: 1

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 316;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 AGAAGAA 139

DB 138 AGAAGAA 145

RESULT 11

T01201

hypothetical protein F21E10.13 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999

C/Accession: T01201

R:Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D.

submitted to the EMBL Data Library, April 1998

A:Description: The sequence of A. thaliana F21E10.

A:Reference number: Z14258

A:Accession: T01201

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-396 <NAV>

A:Cross-references: EMBL:AF058914; NID:93047074; PID:93047085; GSPDB:GN00063; ATSP:F21E10

C:Genetics:

A:Gene: ATSP:F21E10.13

A:Map position: 5

A:Introns: 54/1; 101/2; 196/3; 274/3

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 396;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 SVSSSLSS 65

DB 328 SVSSSLSS 335

RESULT 12

D70784

probable Rheske [2Fe-2S] iron-sulfur protein cyob - *Mycobacterium tuberculosis* (strain H

C:Species: *Mycobacterium tuberculosis*

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C/Accession: D70784

R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Condon, R.; Davies, R.; Devlin, K.; Gentles, S.; Hamlin, N.; Holtroyd, S.

Rajendram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: D70784

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-429 <COL>

A:Cross-references: GB:Z70283; GB:AL123456; NID:93261561; PIDN:CAA94264.1; PID:6233571.

A:Experimental source: strain H3/RV

C:Genetics:

A:Gene: qcrA

C:Superfamily: Rheske [2Fe-2S] homology
C:Keywords: 2Fe-2S; metalloprotein; Rheske iron-sulfur protein
F:343-389/Domain: Rheske [2Fe-2S] homology <RSF>
F:353,355,372,375/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #stat

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 429;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 LGRVYKRK 83

DB 329 LGRVYKRK 336

RESULT 13

I56896

gene gfi-2: protein - rat

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C/Accession: I56896

R:Pinbacher, M.M.; Bear, S.E.; Tschlis, P.N.

J. Virol. 68, 7709-7716, 1994

A:Title: Replacement of interleukin-2 (IL-2)-generated mitogenic signals by a mink c

ed leukemogenesis.

A:Reference number: I56896; PMID:95055995; PMID:7866560

A:Accession: I56896

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <RSS>

A:Cross-references: GB:I56459; NID:9598371; PIDN:AAA63702.1; PID:9598372

C:Genetics:

A:Gene: gfi-2

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 467;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 GARRAGPO 40

DB 327 GARRAGPO 334

RESULT 14

A45268

interleukin-9 receptor precursor - mouse

C:Species: *Mus musculus* (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999

C/Accession: A45268

R:Renaldi, J.C.; Druet, C.; Kermouni, A.; Housiau, F.; Dyttenhove, C.; Van Roost, E.

Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992

A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.

A:Reference number: A45268; PMID:92302307; PMID:1376929

A:Accession: A45268

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-468 <REN>

A:Cross-references: GB:N84746; NID:9194044; PIDN:AAA37871.1; PID:9194045

A:Note: authors translated the codon GGG for residue 394 as Glu

C:Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 468;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 GARRAGPO 40

DB 328 GARRAGPO 335

RESULT 15

G86455

hypothetical protein T1609.7 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C/Accession: G86455
R/Phenology: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:1130712
A/Accession: G86455
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-639 <STO>
A/Cross-references: GB:AE005172; NID:g11054708; PIDN:AG27902.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1

Query Match 3.1%; Score 8; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 SSSLSSE 67
| | | | | | | | | |
DB 79 SSSLSSE 86

Search completed: June 19, 2003, 10:47:16
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:46:36 ; Search time: 21 Seconds
(without alignments)
1319.093 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VNQAPECRFGGIGLPLGKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: GIGG
Gapop: 60.0, Gapext: 60.0

Searched: 417779 seqs, 108206813 residues

Word size: 0

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCN_NEM_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	256	10 US-09-933-814-2	Sequence 2, App1
2	256	100.0	256	10 US-09-824-134-2	Sequence 2, App1
3	74	28.9	74	9 US-10-112-793-25	Sequence 25, App1
4	74	28.9	74	9 US-10-287-354-5	Sequence 5, App1
5	62	24.2	62	12 US-10-035-408-5	Sequence 5, App1
6	52	20.3	84	10 US-09-952-768-64	Sequence 64, App1
7	51	19.9	82	10 US-10-001-254-39	Sequence 39, App1
8	49	19.1	81	10 US-09-410-194-9	Sequence 9, App1
9	45	17.6	77	9 US-10-001-254-35	Sequence 35, App1
10	8	3.1	128	9 US-10-013-379-7	Sequence 7, App1
11	8	3.1	128	9 US-10-013-379-8	Sequence 8, App1
12	8	3.1	311	12 US-10-062-254-288	Sequence 288, App
13	8	3.1	464	9 US-09-764-891-3991	Sequence 3991, App
14	8	3.1	468	10 US-09-965-313-8	Sequence 8, App1
15	8	3.1	502	10 US-09-791-378-672	Sequence 672, App
16	8	3.1	537	9 US-10-184-644-459	Sequence 459, App
17	8	3.1	537	9 US-10-184-634-459	Sequence 459, App
18	8	3.1	610	9 US-10-123-155-493	Sequence 493, App
19	8	3.1	683	9 US-09-738-626-6961	Sequence 6961, App

20	8	3.1	902	9 US-10-184-644-303	Sequence 303, App
21	8	3.1	902	9 US-10-184-634-303	Sequence 303, App
22	8	3.1	997	9 US-10-184-644-23	Sequence 23, App1
23	8	3.1	997	9 US-10-184-634-23	Sequence 23, App1
24	8	3.1	1027	9 US-10-184-644-127	Sequence 127, App
25	8	3.1	1027	9 US-10-184-634-127	Sequence 127, App
26	8	3.1	1106	9 US-10-184-644-535	Sequence 535, App
27	8	3.1	1106	9 US-10-184-634-535	Sequence 535, App
28	8	3.1	1121	9 US-10-123-155-23	Sequence 23, App1
29	8	3.1	1158	9 US-10-184-644-437	Sequence 437, App
30	8	3.1	1158	9 US-10-184-634-437	Sequence 437, App
31	8	3.1	1220	9 US-10-184-644-557	Sequence 557, App
32	8	3.1	1220	9 US-10-184-634-557	Sequence 557, App
33	8	3.1	1305	9 US-10-123-155-803	Sequence 303, App
34	8	3.1	1346	9 US-10-123-155-481	Sequence 481, App
35	8	3.1	1376	9 US-10-123-155-161	Sequence 161, App
36	8	3.1	1449	9 US-10-184-644-375	Sequence 375, App
37	8	3.1	1449	9 US-10-184-634-375	Sequence 375, App
38	8	3.1	1496	9 US-10-123-155-287	Sequence 287, App
39	8	3.1	1514	9 US-10-123-155-329	Sequence 329, App
40	8	3.1	1523	9 US-10-123-155-429	Sequence 429, App
41	8	3.1	1547	9 US-10-123-155-11	Sequence 11, App1
42	8	3.1	1579	9 US-10-184-644-441	Sequence 441, App
43	8	3.1	1579	9 US-10-184-634-441	Sequence 441, App
44	8	3.1	1671	9 US-10-184-644-505	Sequence 505, App
45	8	3.1	1671	9 US-10-184-634-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-09-933-814-2
Sequence 2, Application US/09933814
Patent No. US20020058798A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VAREFOLOMEY, Eugene
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1 RECEPTORS
FILE REFERENCE: WALLACH-16B
CURRENT APPLICATION NUMBER: US/09/933,814
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/860,082
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: PCT/US95/16542
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: IL 112022
PRIOR FILING DATE: 1994-12-15
PRIOR APPLICATION NUMBER: IL 112692
PRIOR FILING DATE: 1995-02-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-09-933-814-2
Query Match
Best Local Similarity 100.0%; Score 256; DB 10; Length 256;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
1 VNQAPECRFGGIGLPLGKRDLARASPPREGARRAGOPRPLADPMPDFVLLSHVS 60
61 SSLSSELTETKFCICGRVYRKLERVOSGIDLSMLEQNDLPFGTELLRETLASLR 120
61 SSLSSELTETKFCICGRVYRKLERVOSGIDLSMLEQNDLPFGTELLRETLASLR 120
61 SSLSSELTETKFCICGRVYRKLERVOSGIDLSMLEQNDLPFGTELLRETLASLR 120
121 HDLRRDDPFGAAGAAAGABEDLCAFNVCNKGDKRRLAROLKVSOTKIDSIEDR 180

Db 121 HDLRRVDDPEAAGAAAGAEEDLCAAFVVICDNGKMRRLAROLKTSDFTRIDSIEDR 180
QY 181 YPRNLTERVESLRIRKNTKEKENVATVAHLVGLRSCOMNLVADLYOEVOQARLQNRSGA 240
Db 181 YPRNLTERVESLRIRKNTKEKENVATVAHLVGLRSCOMNLVADLYOEVOQARLQNRSGA 240
QY 241 MSPSMNSDASTSEAS 256
Db 241 MSPSMNSDASTSEAS 256

RESULT 2
US-09-824-134-2
Sequence 2, Application US/09824134
Patent No. US20020082401A1

GENERAL INFORMATION:
APPLICANT: WALDICH, David
BOLDIN, Mark
VARPOLOMEEV, Eugene
METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,134
FILING DATE: 03-Apr-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/860,082
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-16
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-134-2

Query Match 100.0%; Score 256; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNAPBPCRFGGGIGIPGKRDRLARASEPRREGARRAGPOPRPLADADMOPEVLISYS 60
Db 1 VNAPBPCRFGGGIGIPGKRDRLARASEPRREGARRAGPOPRPLADADMOPEVLISYS 60
QY 61 SSLSSELTELKFLCGLGRVYRKLERVOSGLDFSMLEONDLBPHGTELLRELLASLR 120

Db 61 SSLSSELTELKFLCGLGRVYRKLERVOSGLDFSMLEONDLBPHGTELLRELLASLR 120
QY 121 HDLRRVDDPEAAGAAAGAEEDLCAAFVVICDNGKMRRLAROLKTSDFTRIDSIEDR 180
Db 121 HDLRRVDDPEAAGAAAGAEEDLCAAFVVICDNGKMRRLAROLKTSDFTRIDSIEDR 180
QY 181 YPRNLTERVESLRIRKNTKEKENVATVAHLVGLRSCOMNLVADLYOEVOQARLQNRSGA 240
Db 181 YPRNLTERVESLRIRKNTKEKENVATVAHLVGLRSCOMNLVADLYOEVOQARLQNRSGA 240
QY 241 MSPSMNSDASTSEAS 256
Db 241 MSPSMNSDASTSEAS 256

RESULT 3
US-10-112-793-25
Sequence 25, Application US/10112793
Publication No. US20020192739A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-112-793-25

Query Match 28.9%; Score 74; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.4e-60;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDVVGQDMVRLARQLVSDTKIDSIEDRYPRNTERVESLRIRKNTKEKENVATVAHLV 211
Db 1 ICDVVGQDMVRLARQLVSDTKIDSIEDRYPRNTERVESLRIRKNTKEKENVATVAHLV 211
QY 212 ALRSCOMNLVADLY 225
Db 212 ALRSCOMNLVADLY 225
QY 61 ALRSCOMNLVADLY 74

RESULT 4
US-10-287-594-5
Sequence 5, Application US/10287594
Publication No. US20030096288A1
GENERAL INFORMATION:
APPLICANT: N1, Jian
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: RAIDD, A No. US20030096288A1a1 Death Adaptor Molecule
FILE REFERENCE: 1488.0860002
CURRENT APPLICATION NUMBER: US/10/287,594
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US/09/545,605
PRIOR FILING DATE: 2001-04-07
PRIOR APPLICATION NUMBER: 08/995,159
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-594-5

Query Match
Best Local Similarity 28.9%; Score 74; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4,4e-60;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDWVGKDWRLARLQKVSPTKIDSIEDRYPRNLTERTVRESLRITKNTKRNATVAHLVG 211
DB 1 ICDWVGKDWRLARLQKVSPTKIDSIEDRYPRNLTERTVRESLRITKNTKRNATVAHLVG 60

QY 212 ALRSCOMLVADLV 225
DB 61 ALRSCOMLVADLV 74

RESULT 5
US-10-035-408-5
Sequence 5, Application US/10035408
Patent No. US20020123117A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark P.
VARFOLOMEYEV, Eugene E.
PANCER, Zeev
METT, Igor
GONCHAROV, Tanya M.
WEINMURZEL, Henry
TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROADY AND NETMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/035,408
FILING DATE: 04-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
APPLICATION NUMBER: IL 112,742

FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROADY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-035-408-5

Query Match
Best Local Similarity 24.2%; Score 62; DB 12; Length 62;
Best Local Similarity 100.0%; Pred. No. 3,4e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 WRRLARLQKVSPTKIDSIEDRYPRNLTERTVRESLRITKNTKRNATVAHLVGALSCOMN 219
DB 1 WRRLARLQKVSPTKIDSIEDRYPRNLTERTVRESLRITKNTKRNATVAHLVGALSCOMN 60

QY 220 LV 221
DB 61 LV 62

RESULT 6
US-09-952-768-64
Sequence 64, Application US/09952768
Patent No. US20020035242A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note="human FADD"
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-952-768-64

Query Match      20.3%; Score 52; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 6e-40;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDFEA 132
DB      33 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDFEA 84

RESULT 7
US-10-001-254-39
; Sequence 39, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Steiner-Ilsewen, Frank
; TITLE OF INVENTION: NO. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-39

Query Match      19.9%; Score 51; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.8e-39;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDFEE 131
DB      31 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDFEE 81

RESULT 8
US-09-410-194-9
; Sequence 9, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Immler, Marten
; APPLICANT: Kahne, Michael
; APPLICANT: Schrotter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
```

```

; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-9

Query Match      19.1%; Score 49; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.2e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDD 129
DB      33 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRRVDD 81

RESULT 9
US-10-001-254-35
; Sequence 35, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Steiner-Ilsewen, Frank
; TITLE OF INVENTION: NO. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-35

Query Match      17.6%; Score 45; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRR 125
DB      33 KRRLERVQSGIDLFMSMLEQNDLEPGHTELLRELLASLRHDDLRR 77

RESULT 10
US-10-013-379-7
; Sequence 7, Application US/10013379
; Publication No. US20020188108A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Cate, Jamie H.
; APPLICANT: No. US20020188108A1e1, Harry F.
; APPLICANT: Yusupova, Marat M.
; APPLICANT: Yusupova, Guinara ZH
```

APPLICANT: Baucum, Albion
APPLICANT: Lancaster, Laura
TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAs
FILE REFERENCE: 19629-7010
CURRENT APPLICATION NUMBER: US/10/013,379
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 60/254,603
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 128
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
OTHER INFORMATION: 50S ribosomal protein L7
OTHER INFORMATION: 191Y1
US-10-013-379-7

Query Match
Best Local Similarity 100.0%; Score 8; DB 9; Length 128;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 132 AGAAGAA 139
Db 45 AGAAGAA 52

RESULT 11
US-10-013-379-8
Sequence 8, Application US/10013379
Publication No. US20020188108A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Cate, Jamie H.
APPLICANT: NO. US20020188108A1, Harry F.
APPLICANT: Yusupov, Marat M.
APPLICANT: Yusupova, Gulnara ZH
APPLICANT: Baucum, Albion
APPLICANT: Lancaster, Laura
APPLICANT: Dallas, Anne
TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAs
FILE REFERENCE: 19629-7010
CURRENT APPLICATION NUMBER: US/10/013,379
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 60/254,603
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 128
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
OTHER INFORMATION: 50S ribosomal protein L12
OTHER INFORMATION: 191Y3
US-10-013-379-8

Query Match
Best Local Similarity 100.0%; Score 8; DB 9; Length 128;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 132 AGAAGAA 139
Db 45 AGAAGAA 52

RESULT 12
US-10-062-254-288
Sequence 288, Application US/10062254
Patent No. US20020138882A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yixen
APPLICANT: Hanke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/062,254
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/630,346
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/156899
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/169767
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171054
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/172958
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/171515
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 60/173535
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 288
LENGTH: 311
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-062-254-288

Query Match
Best Local Similarity 100.0%; Score 8; DB 12; Length 311;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 132 AGAAGAA 139
Db 252 AGAAGAA 259

RESULT 13
US-09-764-891-3991
Sequence 3991, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:


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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3991
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (310)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (397)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (399)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3991

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Query Match          3.18; Score 8; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      132 AGAAGAA 139
DB      284 AGAAGAA 291

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RESULT 14
US-09-965-313-8
Sequence 8; Application US/09965313
Patent No. US2002090680A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. US2002090680A1 IL-9/IL-2 Receptor-Like Molecules
FILE REFERENCE: 5800-17A
CURRENT APPLICATION NUMBER: US/09/965,313
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 09/313,913
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 468
TYPE: PRT
ORGANISM: Mus musculus
US-09-965-313-8

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Query Match          3.18; Score 8; DB 10; Length 468;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      33 GARRAGPQ 40
DB      328 GARRAGPQ 335

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```

RESULT 15
US-09-791-378-672
Sequence 672; Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: US/09/791,378

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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 672
LENGTH: 502
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-378-672

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Query Match          3.18; Score 8; DB 10; Length 502;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      135 AAGAAPE 142
DB      115 AAGAAPE 122

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Search completed: June 19, 2003, 10:54:23
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 19, 2003, 10:45:36 ; Search time 26 Seconds

(Without alignments)
289,703 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 256
Sequence: 1 VNOAPECRFGGILGPIGKR.....RSGAMSPMWNDASTSEAS 256

Scoring table: OLIGO

Gapop: 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued: Patents.AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	256	4	US-08-983-502-2
2	256	100.0	256	5	PCT-US95-16542-2
3	256	100.0	256	5	PCT-US96-10521-2
4	208	81.2	208	1	US-08-618-164-3
5	176	68.8	208	4	US-09-074-044A-19
6	114	44.5	201	4	US-09-064-414-2
7	108	42.2	208	4	US-09-064-414-6
8	108	44.5	201	4	US-09-064-414-4
9	100	39.1	208	4	US-09-382-155-19
10	85	33.2	85	4	US-09-042-785A-28
11	74	28.9	74	4	US-08-995-159-5
12	74	28.9	74	4	US-08-828-663A-25
13	62	24.2	62	4	US-08-894-626-5
14	52	20.3	84	1	US-08-665-220-64
15	52	20.3	84	4	US-09-291-692-64
16	51	19.9	83	4	US-09-382-155-15
17	51	19.9	83	4	US-09-074-044A-15
18	31	3.1	379	1	US-08-164-614A-8
19	8	3.1	379	2	US-08-456-489B-8
20	8	3.1	468	2	US-08-164-614A-7
21	8	3.1	468	2	US-08-456-489B-7
22	7	2.7	22	3	US-08-940-095-40
23	7	2.7	22	3	US-08-940-093-40
24	7	2.7	22	3	US-08-940-096-40
25	7	2.7	22	4	US-09-465-719-40
26	7	2.7	22	4	US-09-453-605-40
27	7	2.7	22	4	US-09-453-838-40

28	7	2.7	47	1	US-08-209-747-24	Sequence 24, Appl
29	7	2.7	47	1	US-08-209-747-26	Sequence 26, Appl
30	7	2.7	47	1	US-08-458-298-24	Sequence 26, Appl
31	7	2.7	47	1	US-08-458-298-26	Sequence 26, Appl
32	7	2.7	48	1	US-08-209-747-21	Sequence 21, Appl
33	7	2.7	48	1	US-08-458-298-21	Sequence 21, Appl
34	7	2.7	49	1	US-08-209-747-32	Sequence 22, Appl
35	7	2.7	49	1	US-08-458-298-32	Sequence 22, Appl
36	7	2.7	50	1	US-08-209-747-27	Sequence 27, Appl
37	7	2.7	50	1	US-08-458-298-27	Sequence 27, Appl
38	7	2.7	51	1	US-08-209-747-20	Sequence 20, Appl
39	7	2.7	51	1	US-08-209-747-30	Sequence 20, Appl
40	7	2.7	51	1	US-08-458-298-30	Sequence 30, Appl
41	7	2.7	51	1	US-08-458-298-30	Sequence 30, Appl
42	7	2.7	54	1	US-08-209-747-29	Sequence 29, Appl
43	7	2.7	54	1	US-08-458-298-29	Sequence 29, Appl
44	7	2.7	55	1	US-08-209-747-10	Sequence 10, Appl
45	7	2.7	55	1	US-08-209-747-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-983-502-2
Sequence 2, Application US/08983502
Patent No. 639327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Taty V. GOLITSKY
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-2

Query Match 100.0%; Score 256; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRRGGGILGFLGRRLDARASEPRTGARRAGOPPLADPADPFLVLLHSVS 60
DB 1 VNOAPECRRGGGILGFLGRRLDARASEPRTGARRAGOPPLADPADPFLVLLHSVS 60
QY 61 SLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRLASLR 120
DB 61 SLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRLASLR 120
QY 121 HLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRLAROLKYSDFKIDSIEDR 180
DB 121 HLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRLAROLKYSDFKIDSIEDR 180
QY 181 YPRNLTERVRESIRIKNTEKENATVAHLVGLRSCOMLVADLVOEQARDLQNRSGA 240
DB 181 YPRNLTERVRESIRIKNTEKENATVAHLVGLRSCOMLVADLVOEQARDLQNRSGA 240
QY 241 MSPMWSNDSASTSEAS 256
DB 241 MSPMWSNDSASTSEAS 256

RESULT 2

PCT-US95-16542-2
Sequence 2, Application PC/TUS9516542

GENERAL INFORMATION:
APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
APPLICANT: WEINMORZEL, Henry
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VARELOMEY, Eugene
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
STATE: D.C.
CITY: Washington
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16542
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16542-2

Query Match 100.0%; Score 256; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 4e-233;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRRGGGILGFLGRRLDARASEPRTGARRAGOPPLADPADPFLVLLHSVS 60
DB 1 VNOAPECRRGGGILGFLGRRLDARASEPRTGARRAGOPPLADPADPFLVLLHSVS 60
QY 61 SLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRLASLR 120
DB 61 SLSSELTELKFLCGRVYKRLERVOGSLDFSLBQNDLEPHTELLRLASLR 120
QY 121 HLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRLAROLKYSDFKIDSIEDR 180
DB 121 HLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRLAROLKYSDFKIDSIEDR 180
QY 181 YPRNLTERVRESIRIKNTEKENATVAHLVGLRSCOMLVADLVOEQARDLQNRSGA 240
DB 181 YPRNLTERVRESIRIKNTEKENATVAHLVGLRSCOMLVADLVOEQARDLQNRSGA 240
QY 241 MSPMWSNDSASTSEAS 256
DB 241 MSPMWSNDSASTSEAS 256

RESULT 3

PCT-US96-10521-2
Sequence 2, Application PC/TUS9610521

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-us96-10521-2

Query Match 100.0%; Score 256; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 4e-233;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNAPCECFGGGILGPKGRDLARASEPTEGARAGPOPRPLADAMPFLVLLSYVS 60
 DB 1 VNAPCECFGGGILGPKGRDLARASEPTEGARAGPOPRPLADAMPFLVLLSYVS 60
 QY 61 SLSSELTELFKLCGRVYRKLERVQSGDLFSLLEQNDLEPGHTELLRELLASLR 120
 DB 61 SLSSELTELFKLCGRVYRKLERVQSGDLFSLLEQNDLEPGHTELLRELLASLR 120
 QY 121 HDLLRRVDDEAGAAAGAEEDLCAAFVYICDNGKDMRRRLARQLKSDTKIDIEDR 180
 DB 121 HDLLRRVDDEAGAAAGAEEDLCAAFVYICDNGKDMRRRLARQLKSDTKIDIEDR 180
 QY 181 YPRNLTERRVESLRITKTEKENATVAHLVGLRSCOMLVADLVQEVQARDLQNRSGA 240
 DB 181 YPRNLTERRVESLRITKTEKENATVAHLVGLRSCOMLVADLVQEVQARDLQNRSGA 240
 QY 241 MSPSMNSDASTSEAS 256
 DB 241 MSPSMNSDASTSEAS 256

RESULT 4
 US-08-618-164-3
 Sequence 3, Application US/08618164
 Patent No. 5712115

GENERAL INFORMATION:

APPLICANT: Hawking, Phillip R.
 APPLICANT: Braxton, Scott Michael
 TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/618,164
 FILING DATE: Herewith
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J
 REGISTRATION NUMBER: 33,954
 REFERENCE/DOCKET NUMBER: PF-0058 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-0195
 TELEFAX: 415-852-0195
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 791038
 US-08-618-164-3

Query Match 81.2%; Score 208; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.9e-188;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSLSSELTELFKLCGRVYRKLERVQSGDLFSLLEQNDLEPGH 108
 DB 1 MDPLVLLHSVSSLSSELTELFKLCGRVYRKLERVQSGDLFSLLEQNDLEPGH 60
 QY 109 ELLELLASLRHDLRRVDDEAGAAAGAEEDLCAAFVYICDNGKDMRRRLARQLK 168
 DB 61 ELLELLASLRHDLRRVDDEAGAAAGAEEDLCAAFVYICDNGKDMRRRLARQLK 120
 QY 169 VSDTKIDIEDRYRNLTERVESLRITKTEKENATVAHLVGLRSCOMLVADLVQEV 228
 DB 121 VSDTKIDIEDRYRNLTERVESLRITKTEKENATVAHLVGLRSCOMLVADLVQEV 180
 QY 229 QCARDLQNRSGAMPMSNSDASTSEAS 256
 DB 181 QCARDLQNRSGAMPMSNSDASTSEAS 208

RESULT 5
 US-09-074-044A-19
 Sequence 19, Application US/09074044A
 Patent No. 6207458

GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M
 APPLICANT: HOOD, LEROY
 TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NR-XB, JNK AND
 TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
 STREET: 2405 GRAND BLVD., SUITE 400
 CITY: KANSAS CITY
 STATE: MISSOURI
 COUNTRY: USA
 ZIP: 64108

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/074,044A
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: COLLINS, JOHN M
 REGISTRATION NUMBER: 26,262
 REFERENCE/DOCKET NUMBER: 26588
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 816/474-9050
 TELEFAX: 816/474-9057
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 ORGANISM: Homo sapiens
 US-09-074-044A-19

Query Match 68.8%; Score 176; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRKIERVOSGLDLSMILEONDEPGTELLRELLASLRHDLRRVDFEAGAAGAP 140
DB 33 KRKIERVOSGLDLSMILEONDEPGTELLRELLASLRHDLRRVDFEAGAAGAP 92
OY 141 GEEDLCAPNVICDNGKDMRRLAROLKVSPTKIDSTEDRPRMLTERVRESLTKMTE 200
DB 93 GEEDLCAPNVICDNGKDMRRLAROLKVSPTKIDSTEDRPRMLTERVRESLTKMTE 152
OY 201 KENATVAHLVGLASCOMNLVADLVQVQARLDQNSGAMSPMSWSDASTSEAS 256
DB 153 KENATVAHLVGLASCOMNLVADLVQVQARLDQNSGAMSPMSWSDASTSEAS 208

RESULT 6
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:

APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-4117
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-2

Query Match 44.5%; Score 114; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRHDLRRVDFEAGAAGAPGEEDLCAPNVICDNGKDMRRLAROLKYSPT 172
DB 58 ELASLRHDLRRVDFEAGAAGAPGEEDLCAPNVICDNGKDMRRLAROLKYSPT 117
OY 173 KIDSIEDRYPRLTERVRESLTKMTEKENATVAHLVGLASCOMNLVADLVQ 226
DB 118 KIDSIEDRYPRLTERVRESLTKMTEKENATVAHLVGLASCOMNLVADLVQ 171

RESULT 7

US-09-064-414-6
Sequence 6, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-4117
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-6

Query Match 44.5%; Score 114; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 HTELLRELLASLRHDLRRVDFEAGAAGAPGEEDLCAPNVICDNGKDMRRLARQ 166
DB 59 HTELLRELLASLRHDLRRVDFEAGAAGAPGEEDLCAPNVICDNGKDMRRLARQ 118
OY 167 LKVSPTKIDSTEDRYPRLTERVRESLTKMTEKENATVAHLVGLASCOMNL 220
DB 119 LKVSPTKIDSTEDRYPRLTERVRESLTKMTEKENATVAHLVGLASCOMNL 172

RESULT 8
US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875

GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 42.2%; Score 108; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 66-94;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ELIASLRHDLRRVDFEAGAAAGPGEEDICAAFNVCIDNVGKDMRLARQLKVSDT 172
DB 58 ELIASLRHDLRRVDFEAGAAAGPGEEDICAAFNVCIDNVGKDMRLARQLKVSDT 117
QY 173 KIDSIERYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSCOML 220
DB 118 KIDSIERYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSCOML 165

RESULT 9
US-09-382-155-19
Sequence 19, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATENTS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-19

Query Match 39.1%; Score 100; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKDMRLARQLKVSDFKIDSIEDRYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSC 216
DB 109 GKDMRLARQLKVSDFKIDSIEDRYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSC 168
QY 217 QMNLVADLVQEQARQLQNRSGAMSPKSNRSDASTSEAS 256
DB 169 QMNLVADLVQEQARQLQNRSGAMSPKSNRSDASTSEAS 208

RESULT 10
US-09-042-785A-28

Sequence 28, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHAYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-09-042-785A-28

Query Match 33.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.2e-72;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 ICAAFNYICDVGDMRLARQLKVSDFKIDSIEDRYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSCOML 204
DB 1 ICAAFNYICDVGDMRLARQLKVSDFKIDSIEDRYPRNLTERRYRESLRIMKNTKRNATVAHLVGLRSCOML 60
QY 205 TVAHVGLRSCOMLTVADLVQEQV 229
DB 61 TVAHVGLRSCOMLTVADLVQEQV 85

RESULT 11
US-08-995-159-5
Sequence 5, Application US/08995159
Patent No. 6130079
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,159
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488, 0860001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2500
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-995-159-5

Query Match 28.9%; Score 74; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-62;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGDMRLAQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENATVAHLVG 211
DB 1 ICDNVGDMRLAQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENATVAHLVG 60

QY 212 ALRSCQMLVADLV 225
DB 61 ALRSCQMLVADLV 74

RESULT 12
US-08-828-683A-25
Sequence 25, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marchand, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-828-683A-25

Query Match 28.9%; Score 74; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-62;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGDMRLAQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENATVAHLVG 211
DB 1 ICDNVGDMRLAQLKVSPTKIDSDRYPRNTERVRESLRIMKTEKENATVAHLVG 60

QY 212 ALRSCQMLVADLV 225
DB 61 ALRSCQMLVADLV 74

RESULT 13
US-08-894-626-5
Sequence 5, Application US/08894626
Patent No. 635780
GENERAL INFORMATION:

APPLICANT: WALLACH, David
BOLDIN, Mark P.
VAROLIOEV, Eugene E.
PANCER, Zeev
METZ, Igor
GONCHAROV, Tanya M.
WEINMURZEL, Henry

TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-08-694-626-5

Query Match 24.2%; Score 62; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9e-51;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 160 WRRLAROLKVSDFKIDSEIDRYPRNLTREYRESLRIRKNTKEKATVAHLVGLRSCOM 219
1 WRRLAROLKVSDFKIDSEIDRYPRNLTREYRESLRIRKNTKEKATVAHLVGLRSCOM 60

QY 220 LV 221
DB 61 LV 62

RESULT 14
US-08-665-220-64
Sequence 64, Application US/08665220
Patent No. 5786173

GENERAL INFORMATION:

APPLICANT: Alnemir, Ema S.
APPLICANT: Fernandes-Alnemir, Teresa

APPLICANT: Litwack, Gerald

APPLICANT: Armstrong, Robert

APPLICANT: Tomaseilli, Kevin

TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,

TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,220

FILING DATE: 14-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/618,408

FILING DATE: 19-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human FADD"

US-08-665-220-64

Query Match 20.3%; Score 52; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLRYVSGDLTFSMLLEQNDLEPGHTELLRELLASLRRDDLLRRVDFFEA 132
DB 33 KRKLRYVSGDLTFSMLLEQNDLEPGHTELLRELLASLRRDDLLRRVDFFEA 84

RESULT 15
US-09-291-692-64
Sequence 64, Application US/09291692
Patent No. 6287795

GENERAL INFORMATION:

APPLICANT: Alnemir, Ema S.

APPLICANT: Fernandes-Alnemir, Teresa

APPLICANT: Litwack, Gerald

APPLICANT: Armstrong, Robert

APPLICANT: Tomaseilli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED AND BERRY

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: Use

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,692

FILING DATE: 04-13-1999

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human FADD"

US-09-291-692-64

Query Match 20.3%; Score 52; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRKLRYVSGDLTFSMLLEQNDLEPGHTELLRELLASLRRDDLLRRVDFFEA 132
DB 33 KRKLRYVSGDLTFSMLLEQNDLEPGHTELLRELLASLRRDDLLRRVDFFEA 84

Search completed: June 19, 2003, 10:53:03
Job time : 27 secs

PA (WEIN/) WEINWURZEL H.

PA (WEIN/) WEINURZEL H.
PA (YEDA) YEDA RES & DEV CO LTD

XX Boldin M, Golitsev YV, Goncharov T, Wallach D;
 XX WPI, 1997-122570/12.
 DR N-PSDB; AAT01397.
 XX
 PT New DNA encoding MACH protein that interacts with MORT-1 protein
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX
 PS Disclosure; Page 102-103; 163pp; English.

CC This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAM11892), designated MACH. MORT-1 binds to the FAS ligand receptor
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p55-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.

SO Sequence 256 AA;

Query Match 100.0%; Score 256; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.1e-233;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNAPPCRFGGGILGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 60
 DB 1 VNAPPCRFGGGILGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 60
 QY 61 SLSSESELELTKFCIGRVYKRLERVOGSLDFSMLEONDEPHTELLRELLASLR 120
 DB 61 SLSSESELELTKFCIGRVYKRLERVOGSLDFSMLEONDEPHTELLRELLASLR 120
 QY 121 HDLLRRVDDFEAGAAAGAAAGPGEEDLCAAFNVICDNGKDWRRRLAROLKVSPTKIDSIEDR 180
 DB 121 HDLLRRVDDFEAGAAAGAAAGPGEEDLCAAFNVICDNGKDWRRRLAROLKVSPTKIDSIEDR 180
 QY 181 YPNLTERVRESLRINKNTEKENATVAHLVGLALSCOMNTVADLYOEVOQARDLQNSGA 240
 DB 181 YPNLTERVRESLRINKNTEKENATVAHLVGLALSCOMNTVADLYOEVOQARDLQNSGA 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 MSPMSWNSDASTSEAS 256

RESULT 2
 AAR98346
 ID AAR98346 standard; Protein; 256 AA.

XX AAR98346;

XX 13-SEP-1996 (first entry)

XX MORT-1 modulator of FAS receptor.

XX MORT-1, HFL, FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 KM mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Domain 160..221
 FT /label= Death domain

XX W09618641-A1.

XX 20-JUN-1996.

XX 14-DEC-1995; 95MO-US16542.

XX 16-JUL-1995; 95IL-0114615.

XX 15-DEC-1994; 94IL-0112022.

XX 19-FEB-1995; 95IL-0112692.

XX (WEIN/) WEINMURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.

XX Boldin M, Mett I, Varfolomeev E, Wallach D;

XX WPI, 1996-300569/30.

XX N-PSDB; AAT30372.

XX MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells

XX Claim 5; Fig 4; 72pp; English.

CC MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFL,
 CC is a novel protein that binds to the intracellular domain (Fas-IC) of
 CC the Fas ligand receptor Fas-R (or Fas/APOL), and is capable of
 CC modulating the function of Fas-R. MORT-1 is also capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from Hela cells.
 CC MORT-1 can be used to modulate the Fas-R ligand on cells carrying
 CC an Fas-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.

SO Sequence 256 AA;

Query Match 99.6%; Score 255; DB 17; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.8e-232;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NOAPECRFFGGGILGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 61

DB 2 NOAPECRFFGGGILGPGKRRDLARASEPTREGARRAGPPRRPLADPAMPDFVLLHSVS 61

QY 62 SLSSESELELTKFCIGRVYKRLERVOGSLDFSMLEONDEPHTELLRELLASLR 121

DB 62 SLSSESELELTKFCIGRVYKRLERVOGSLDFSMLEONDEPHTELLRELLASLR 121

QY 122 DLRRVDDFEAGAAAGAAAGPGEEDLCAAFNVICDNGKDWRRRLAROLKVSPTKIDSIEDR 181

DB 122 DLRRVDDFEAGAAAGAAAGPGEEDLCAAFNVICDNGKDWRRRLAROLKVSPTKIDSIEDR 181

QY 182 PNLTERVRESLRINKNTEKENATVAHLVGLALSCOMNTVADLYOEVOQARDLQNSGA 241

DB 182 PNLTERVRESLRINKNTEKENATVAHLVGLALSCOMNTVADLYOEVOQARDLQNSGA 241

QY 242 SPMMSWNSDASTSEAS 256

DB 242 SPMMSWNSDASTSEAS 256

RESULT 3
 AAY51329
 ID AAY51329 standard; Protein; 208 AA.

XX

AAV51329;
19-APR-2000 (first entry)
Human FADD protein.
FADD; human; antisense; inhibitor; Fas-associated death domain.
Homo sapiens:
US6015712-A.
18-JAN-2000
19-JUL-1999; 99US-0357072.
19-JUL-1999; 99US-0357072.
(ISIS-) ISIS PHARM INC.
Monta BP, Covert LM, Baker BF, Zhang H;
WPI: 2000-126316/11.
N-PSDB; AA244745.
Antisense oligonucleotides, useful for inhibiting human Fas-associated death domain (FADD) expression are targeted to the 3' untranslated region of the FADD gene.
Example 13; Column 43-46; 37pp; English.
This invention describes novel antisense oligonucleotides (OGNs) (1) 8-20 nucleotides in length that specifically hybridize with and inhibit nucleic acids encoding human Fas-associated death domain (FADD), targeted to the 3' untranslated region (3'UTR). (1) can be used to treat animals, especially humans, suspected of having or being prone to a disease or condition associated with FADD expression. This sequence represents the human FADD protein described in the method of the invention.
Sequence 208 AA:
SQ
Query Match 81.2%; Score 208; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-188; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
49 MDPEVLLHSVSSSSSELTEKELGKLVKRLERVOGSLDFSMLEQNDEPGHT 108
1 MDPEVLLHSVSSSSSELTEKELGKLVKRLERVOGSLDFSMLEQNDEPGHT 60
109 ELRELRLASLRHHDLRRVDFEAGAAAGAAPGEEDLCAAFNVICDNYGKDMRLAROLK 168
61 ELRELRLASLRHHDLRRVDFEAGAAAGAAPGEEDLCAAFNVICDNYGKDMRLAROLK 120
169 VSDPTIDSIDERYPRNLTERRPRESIRIKNTEKENATVAHLVGAIRSCQMTVALDVG 228
121 VSDPTIDSIDERYPRNLTERRPRESIRIKNTEKENATVAHLVGAIRSCQMTVALDVG 180
229 QOARDLQNRSGAMSPMNSDASTSEAS 256
181 QOARDLQNRSGAMSPMNSDASTSEAS 208
RESULT 4
AAW03653
ID AAW03653 standard; Protein; 208 AA.
AAW03653;
22-FEB-1997 (first entry)
FADD (Fas-associating protein with novel death domain) protein..

Human; FADD; Fas-associating protein with novel death domain;
apoptosis; Fas receptor; death domain; gene therapy; antibody;
immunossay; drug screening; diagnostic; AIDS; antiinflammatory;
antitumour; cerebroprotective; neuroprotective.
Homo sapiens.
Key Location/Qualifiers
Region 1..125 "N-terminal fragment, inducing apoptosis but not binding to Fas receptor"
Region 35..208 /note= "C-terminal active fragment"
Region 41..208 /note= "C-terminal active fragment"
Region 42..208 /note= "Fas receptor-binding NFD-2 polypeptide"
Region 61..208 /note= "Fas receptor-binding NFD-3 polypeptide"
Region 80..208 /note= "Fas receptor-binding NFD-4 polypeptide"
Misc-difference 121 /note= "Altered to Asn in FADDmt mutant"
Domain 111..177 /note= "Death domain"
W09631603-A2.
10-OCT-1996.
28-FEB-1996; 96MO-US02857.
18-MAY-1995; 95US-0443982.
03-APR-1995; 95US-0416379.
(UNMI) UNIV MICHIGAN.
Dixit VM, O'Rourke K;
WPI: 1996-465026/46.
N-PSDB; AAT39397.
FADD protein that binds to cytoplasmic region of Fas receptor - for identifying inhibitors of Fas-associated apoptosis useful for treating e.g. AIDS, leukaemia, stroke, etc
Example 1; Fig 2A-B; 96pp; English.
The sequence corresponds to FADD (Fas-associating protein with novel death domain), which binds the cytoplasmic region of a Fas receptor, and modulates apoptosis induced by activation of the receptor by ligand binding. The FADD cDNA has been isolated using a yeast two-hybrid system to screen for proteins interacting with the Fas cytoplasmic domain. The protein contains a death domain, with interacts with the death domain of Fas. Mutation of Val-121 to Asn in mutant FADDmt disrupts binding and/or signalling properties. C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor cytoplasmic domain in vitro. An N-terminal fragment induces apoptosis but does not bind the Fas receptor. The encoding DNA may be used in gene therapy, and the protein or a corresponding antibody may be used to screen for agents modulating FADD pathway cellular functions and Fas-associated apoptosis, for use in therapy of e.g. AIDS, inflammation, leukaemia, myocardial infarction, degenerative disease, etc.
Sequence 208 AA:
SQ
Query Match 68.8%; Score 176; DB 17; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158; Indels 0; Gaps 0;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
81 KRRLERVOGSLDFSMLEQNDEPGHTELRRLASLRHHDLRRVDFEAGAAAGAP 140

DB 33 KRRLERVOSGLDLSMLLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 92
QY 141 GEEDLCAAFNVICDNGKDMRRLAROLKVSDFKIDSIEDRYPNLTERVESIRIKNTE 200
DB 93 GEEDLCAAFNVICDNGKDMRRLAROLKVSDFKIDSIEDRYPNLTERVESIRIKNTE 152
QY 201 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 256
DB 153 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 208

RESULT 5
AAM96154
ID AAM96154 standard; Protein; 208 AA.
AC AAM96154;
XX 27-APR-1999 (first entry)
DT Human FADD protein.
XX
DE
XX FIP; FADD interacting protein; FADD; Fas-associated protein with a
XX novel death domain; cell death; apoptosis; Alzheimer's disease;
XX Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
XX amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
XX protozoa; neoplasia; dysplasia; hyperplasia.
XX Homo sapiens.
XX OS
XX MO9900499-A1.
XX PD 07-JAN-1999.
XX 26-JUN-1998; 98MO-US13320.
XX 03-JUN-1998; 98US-0087886.
XX 26-JUN-1997; 97US-0050792.
XX (CHTR) CHIRON CORP.
XX Chen TT, Williams LT;
XX MPI; 1999-095745/08.
XX N-PSDB; AAX08910.
XX
XX New FADD (Fas-associated protein with a novel death
XX domain)-Interacting Protein - useful for inducing or preventing
XX apoptosis in a cell, to aid in controlling apoptosis-related
XX diseases
XX
XX Disclosure: Page 47; 58pp; English.

XX An epitope of human FADD (Fas-associated protein with a novel
XX death domain)-Interacting protein (FIP protein) comprising amino
XX acids 348-727 of the protein described in AAM96153, can be used to
XX induce or prevent apoptosis in a cell. Specifically, decreasing the
XX levels of FIP348-727 prevents apoptosis. This is useful in cells
XX which are dying prematurely, eg: Alzheimer's disease, Acquired
XX Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic
XX lateral sclerosis (and other muscle wasting diseases), autoimmune
XX diseases, and diseases where cells are infected with a pathogen
XX (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the
XX levels of FIP 348-727 induces apoptosis which is useful in cells
XX suffering from neoplasias, dysplasias, hyperplasias, or their
XX symptoms. Purified and isolated FIP subgenomic polynucleotides are
XX useful as primers to obtain more copies of the nucleotides, and as
XX probes that identify wild-type or mutant coding sequences. They are
XX also useful for expressing FIP mRNA, proteins or fusion proteins,
XX and in the generation of FIP antisense oligonucleotides and
XX ribozymes. They are also useful in expression constructs and in
XX gene delivery vehicles (optionally in combination with a condensing
XX agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
XX (including variants), FIP-specific ribozymes or single-chain

CC antibodies into eukaryotic cells. This is the human FADD protein.
CC Human FIP protein binds to amino acids 1-110 of this sequence.
XX
SQ Sequence 208 AA;
Query Match 68.8%; Score 176; DB 20; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KRRLERVOSGLDLSMLLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 140
DB 33 KRRLERVOSGLDLSMLLEQNDLEPGHTELLRELLASLRHDLRRVDFEAGAAGAP 92
QY 141 GEEDLCAAFNVICDNGKDMRRLAROLKVSDFKIDSIEDRYPNLTERVESIRIKNTE 200
DB 93 GEEDLCAAFNVICDNGKDMRRLAROLKVSDFKIDSIEDRYPNLTERVESIRIKNTE 152
QY 201 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 256
DB 153 KENATVAHLVGLRSCOMNLVADLVQVOQARDLQNRSGAMSPMSNSDASTSEAS 208

RESULT 6

AAB84804
ID AAB84804 standard; Protein; 208 AA.
AC AAB84804;
XX 12-JUL-2001 (first entry)
DT Human FADD prodomain.
XX
DE
XX
XX NF-kappaB; JNK; apoptosis; death effector domain; DED.
XX OS
XX Homo sapiens.
XX OS
XX US6207458-B1.
XX PD 27-MAR-2001.
XX 07-MAY-1998; 98US-0074044.
XX 07-MAY-1998; 98US-0074044.
XX (UNIW) UNIV WASHINGTON.
XX Chaudhary PM, Hood L;
XX MPI; 2001-342087/36.
XX
XX Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
XX activity by comparing cell activity in presence and absence of
XX proteinaceous species having two death effector domain and test
XX compound
XX
XX Disclosure: Column 51-52; 62pp; English.

XX The present invention relates to testing candidate compounds to
XX determine whether they affect NF-kappaB, JNK and apoptosis activity.
XX The method involves the use of 2 death effector domains (DED). The
XX compounds identified by the invention have therapeutic
XX applications and are useful for regulating cellular NF-kappaB, JNK
XX and apoptosis activity. The assay is useful for identifying
XX pharmacological agents or lead compounds generally involved in
XX assaying for compounds which regulate or modulate a cell activity.
XX The present sequence is a prodomain used in the invention.
XX
XX Sequence 208 AA;

Query Match 68.8%; Score 176; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.3e-158;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRKLERSVSGDLEFSLMEONDLPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 140
 DB 33 KRKLERSVSGDLEFSLMEONDLPGHTELLRELLASLRHDLRRVDFEAGAAAGAP 92
 OY 141 GEEDLCAAFNYICDNVGDMPRLAROLKVSPTKIDSIDRYPRNLTERVRESLRIMKTE 200
 DB 93 GEEDLCAAFNYICDNVGDMPRLAROLKVSPTKIDSIDRYPRNLTERVRESLRIMKTE 152
 OY 201 KENATVAHLVGLASCOMNLVADLVQEVQARDLQNRSGAMSPMSNSDASTSEAS 256
 DB 153 KENATVAHLVGLASCOMNLVADLVQEVQARDLQNRSGAMSPMSNSDASTSEAS 208

RESULT 7
 AAW87491
 ID AAW87491 standard; Protein: 201 AA.

AAW87491;
 12-FEB-1999 (first entry)

Amino acid sequence of MOR1 isoform MOR1del21 from NTERA2 cells.

MOR1; MOR1del21; NTERA2; CNS; isoform; death domain; Fas/APOL;
 MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 in vivo agent; neuronal apoptosis; human.

Homo sapiens.

MO8849297-A1.

05-NOV-1998.

14-APR-1998; 98WO-US07439.

25-APR-1997; 97US-0044835.

(AMHP) AMERICAN HOME PROD CORP.

Bingham BW, Birsan C, Wood AT, Young KH;

WPI; 1999-009424/01.

N-PSDB; AAV71928.

Human, neuronal MOR1 iso:form(s) - used as screening agents in
 diagnosing CNS diseases, and in discovering CNS-specific
 anti-apoptotic compounds

Claim 5; Pages 26-27; 31pp; English.

This represents the amino acid sequence of a MOR1 isoform MOR1del21.
 The encoding cDNA was isolated from NTERA2 cells and deposited under the
 accession number ATCC 209013. The cDNA has a 21 base pair deletion as
 compared to the published MOR1 sequence (bp 172-192 of the coding
 sequence). The invention relates to three MOR1 nucleic acid isoforms
 (AAV71928 to AAV71930) that encode proteins which can interact with the
 death domain of Fas/APOL. The MOR1 isoforms can also interact with MACH
 alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 The transcript isoforms, together with their encoded proteins are useful
 as screening agents in diagnosing CNS diseases, and in discovering CNS-
 specific anti-apoptotic compounds. They are useful in gene therapy
 either as in vivo agents in humans or as experimental tools in
 manipulating neuronal apoptosis in cell culture and animal model
 systems.

Sequence 201 AA;

Query Match 44.5%; Score 114; DB 20; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.2e-99;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 ELASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICDNVGDMPRLAROLKVSPT 172

DB 58 ELASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICDNVGDMPRLAROLKVSPT 117
 OY 173 KIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGLASCOMNLVADLVQ 226
 DB 118 KIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGLASCOMNLVADLVQ 171

RESULT 8
 AAW87493
 ID AAW87493 standard; Protein: 208 AA.

AAW87493;
 12-FEB-1999 (first entry)

Amino acid sequence of MOR1 isoform MOR1G173A from human brain.

MOR1; MOR1G173A; NTERA2; CNS; isoform; death domain; Fas/APOL;
 MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 in vivo agent; neuronal apoptosis; human.

Homo sapiens.

MO8849297-A1.

05-NOV-1998.

14-APR-1998; 98WO-US07439.

25-APR-1997; 97US-0044835.

(AMHP) AMERICAN HOME PROD CORP.

Bingham BW, Birsan C, Wood AT, Young KH;

WPI; 1999-009424/01.

N-PSDB; AAV71930.

Human, neuronal MOR1 iso:form(s) - used as screening agents in
 diagnosing CNS diseases, and in discovering CNS-specific
 anti-apoptotic compounds

Claim 7; Pages 30-31; 31pp; English.

This represents the amino acid sequence of a MOR1 isoform MOR1G173A.
 The encoding cDNA was isolated from human brain and deposited under the
 accession number ATCC 209019. The cDNA has a nucleotide substitution (G
 to A) at basepair position 173 of the published MOR1 coding sequence.
 The invention relates to three MOR1 nucleic acid isoforms (AAV71928 to
 AAV71930) that encode proteins which can interact with the death domain
 of Fas/APOL. The MOR1 isoforms can also interact with MACH alpha1 or
 other members of the ICE/Ced3 (Caspase) family of proteins. The
 transcript isoforms, together with their encoded proteins are useful
 as screening agents in diagnosing CNS diseases, and in discovering
 CNS-specific anti-apoptotic compounds. They are useful in gene therapy
 either as in vivo agents in humans or as experimental tools in
 manipulating neuronal apoptosis in cell culture and animal model
 systems.

Sequence 208 AA;

Query Match 44.5%; Score 114; DB 20; Length 208;
 Best Local Similarity 100.0%; Pred. No. 2.3e-99;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICDNVGDMPRLARQ 166

DB 59 HTELLRELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNYICDNVGDMPRLARQ 118

OY 167 LKVSPTKIDSIDRYPRNLTERVRESLRIMKTEKENATVAHLVGLASCOMNL 220

DB 119 LKVSPTKIDSIDRYPRNLTERVRESLRIMKTEKENATVAHLVGLASCOMNL 172

RESULT 9
AAM87492
ID AAM87492 standard; Protein: 201 AA.
XX
AC AAM87492;
XX
DT 12-FEB-1999 (first entry)
XX
DE Amino acid sequence of MOR1 isoform MOR1del21 from human brain.
XX
KM MOR1; MOR1del21; NTERA2; CNS; Isoform; death domain; Fas/AP01;
KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
KV In vivo agent; neuronal apoptosis; human.
OS Homo sapiens.
PM W09849297-A1.
PN
PD 05-NOV-1998.
PE 14-APR-1998; 98WO-US07439.
PF
PR 25-APR-1997; 97US-0044835.
PS (AMHP) AMERICAN HOME PROD CORP.
PT
PI Bingham BW, Birsan C, Wood AT, Young KH;
PP WPI; 1999-009424/O1.
PSDB; AAV71929.
PT Human, neuronal MOR1 isoform(s) - used as screening agents in
PT diagnosing CNS diseases, and in discovering CNS-specific
PT anti-apoptotic compounds
XX
XX Claim 6; Pages 28-29; 31pp; English.
XX
CC This represents the amino acid sequence of a MOR1 isoform MOR1del21.
CC The encoding cDNA was isolated from human brain and deposited under the
CC accession number ATCC 209018. The cDNA has a 21 base pair deletion as
CC compared to the published MOR1 sequence (bp 172-192 of the coding
CC sequence). The invention relates to three MOR1 nucleic acid isoforms
CC (AAV71928 to AAV71930) that encode proteins which can interact with the
CC death domain of Fas/AP01. The MOR1 isoforms can also interact with MACH
CC alpha or other members of the ICE/Ced3 (Caspase) family of proteins.
CC The transcript isoforms, together with their encoded proteins are useful
CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
CC specific anti-apoptotic compounds. They are useful in gene therapy
CC either as in vivo agents in humans or as experimental tools in
CC manipulating neuronal apoptosis in cell culture and animal model
CC systems.
XX
SQ Sequence 201 AA;
XX
Query Match 42.2%; Score 108; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e-93;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 113 ELASLRHHDLIRRYDDEFAGAAAGAPGEEEDLCAAFNYTCNVKDKMRRLAROLKVSDT 172
DB 58 ELASLRHHDLIRRYDDEFAGAAAGAEEDLCAAFNYTCNVKDKMRRLAROLKVSDT 117
OY 173 KIDSTIEDYPRNLTFRVRESRLRMNTKEKNATVAHLVGALRSQCNLT 220
DB 118 KIDSTIEDYPRNLTFRVRESRLRMNTKEKNATVAHLVGALRSQCNLT 165
RESULT 10
AAB61119
ID AAB61119 standard; protein: 208 AA.
XX
AC AAB61119;

Query Match	Best Local Similarity	Score 100;	DB 22;	Length 208;
Matches 100;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0
0y	157 GDMWRRLARQLKVSPTKIDSIEDRYPRNLTREVERRESLRIMKTEKENAVAHVGLALRSC	216		
Db	109 GDMWRRLARQLKVSPTKIDSIEDRYPRNLTREVERRESLRIMKTEKENAVAHVGLALRSC	168		
0y	217 OMNIVADIVQEVQCARDLQNRSGAMSPMSWNSDASTSEAS	256		
Db	169 OMNIVADIVQEVQCARDLQNRSGAMSPMSWNSDASTSEAS	208		
RESULT 11				
AAW00210				
ID	AAW00210 standard; peptide; 62 AA.			
AC	AAW00210;			
XX				
XX	17-APR-1997 (first entry)			
XX				
XX	Human MORF-1 protein death domain motif.			
XX				
XX	Death domain; regulatory protein; NGF-R; nerve growth receptor;			
KM	FAS-R; Fas ligand receptor; Fas/ABO1; ankyrin 1; p53 TNF-R;			
KM	tumour necrosis factor receptor; MORF1; cell cytotoxicity; HIV;			
KM	human immunodeficiency virus; cancer; neoplasia; disease			
XX				
OS	Homo sapiens.			
XX				
XX	US6160095-A.			
XX				
XX	12-DEC-2000;			
PD				
XX	24-AUG-1999; 99US-0382155.			
PE				
XX	07-MAY-1998; 98US-0074044.			
PR				
XX	(UNIV) UNIV WASHINGTON.			
PA	(STOW-) STOWERS INST MEDICAL RES.			
XX				
PI	Hood L, Chaudhary PM;			
XX				
DR	WPI; 2001-101569/11.			
XX				
XX	Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating			
XX	nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,			
PT	for therapeutic purposes			
XX				
XX	Example 8; Fig 11; 60pp; English.			
PS				
XX				
XX	The present sequence has been shown to regulate the nuclear factor-kappa			
CC	B (NF-kB), Jun N-terminal kinase (JNK) and apoptosis pathways. It			
CC	is provided in a specification relating to novel mutants (D73A, L74A and			
CC	L75A) for Caspase-8, which are also useful for regulating NF-kB, JNK			
CC	and apoptosis activities. The Caspase-8 mutants are useful for			
CC	therapeutic purposes and in test methods or assays for determining			
CC	whether a candidate compound has a significant effect upon cell			
CC	activities, especially NF-kB, JNK and apoptosis, so as to facilitate the			
CC	discovery and/or design of therapeutic agents.			
XX				
XX	Sequence 208 AA;			
SQ				

PN W09625941-A1.
 XX
 PD 29-AUG-1996.
 XX
 PF 15-FEB-1996; 96WO-US02326.
 XX
 PR 13-SEP-1995; 95IL-0115289.
 PR 22-FEB-1995; 95IL-0112742.
 XX
 PA (WEIN/) WEINMURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Boidin MP, Goncharov TM, Mett I, Pancer Z, Varfolomeev EE;
 PI Wallach D;
 XX WPI: 1996-402125/40.
 DR
 XX
 PT Modulator of regulatory cellular events mediated by "death domain"
 PT contg. regulatory proteins - useful for modulating functions
 PT mediated in cells by proteins contg the death domain
 XX
 PS Claim 9; Fig 1; 74pp: English.
 CC
 CC AAM00210 shows the death domain of the MORT-1, which binds to the
 CC intracellular portion of the human Fas-ligand receptor (FAS-R). The
 CC death domain (DD) of FAS-R, p55 tumour necrosis factor receptor
 CC (p55 TNF-R), nerve growth factor receptor (NGF-R) and ankyrin 1 are also
 CC given (see AAM00206 and AAM00208-W00210). These Dds are used to identify
 CC compounds capable of modulating activity of the regulatory proteins
 CC (p55, NGF, TNF and FAS-R ligand, MORT-1) via interaction with the Dds.
 CC Such modulators which may be antibodies, antisense sequences or
 CC ribozymes (which can affect the cellular mRNA sequences encoding the
 CC proteins within the cell. Tumour cells, HIV-infected cells or other
 CC diseased cells can be treated by targeting the cells with animal viral
 CC vectors encoding the modulators and a viral surface antigen capable of
 CC binding to a specific receptor. The Dds are characterised by having
 CC groups of common amino acid residues Trp, Ala, Asp, Glu, Thr, Arg and
 CC Tyr within locations that can be aligned to show homology.
 XX
 SQ Sequence 62 AA:
 Query Match 24.2%; Score 62; DB 17; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1e-50;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 160 WRRLAROLKVSPTKIDSTEDRRPRNLTERVRPESLAKMTKEKNTVAHLVGLALSSQNN 219
 DB 1 WRRLAROLKVSPTKIDSTEDRRPRNLTERVRPESLAKMTKEKNTVAHLVGLALSSQNN 60
 OY 220 LV 221
 DB 61 LV 62
 RESULT 12
 AAB84800
 ID AAB84800 standard; Protein; 83 AA.
 XX
 AC AAB84800;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE FADD death effector domain 1.
 XX
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 OS Homo sapiens.
 XX
 PN US6207458-B1.
 PD 27-MAR-2001.
 XX

PF 07-MAY-1998; 98US-0074044.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIM) UNIV WASHINGTON.
 XX
 PI Chaudhary PM, Hood L;
 XX
 DR WPI: 2001-342087/36.
 XX
 PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteinaceous species having two death effector domain and test
 XX compound
 XX
 PS Claim 10; Column 45-47; 62pp; English.
 CC
 CC The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic
 CC applications and are useful for regulating cellular NFkappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.
 CC The present sequence is a death effector domain of the invention.
 XX
 SQ Sequence 83 AA:
 Query Match 19.9%; Score 51; DB 22; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.2e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 81 RKRTRVSGDLFSLLEQNDLEPQHMLRELLASRRHLLRVDDFE 131
 DB 33 RKRTRVSGDLFSLLEQNDLEPQHMLRELLASRRHLLRVDDFE 83
 RESULT 13
 AAB61115
 ID AAB61115 standard; Protein; 83 AA.
 XX
 AC AAB61115;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human FADD DED1 domain.
 XX
 KW Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KW Jun N-terminal kinase; JNK; apoptosis; Caspase-8 mutant;
 KW death effector domain; DED.
 XX
 OS Homo sapiens.
 XX
 PN US6160095-A.
 XX
 PD 12-DEC-2000.
 XX
 PF 24-AUG-1999; 99US-0382155.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIM) UNIV WASHINGTON.
 PA (STOM-) STOMERS INST MEDICAL RES.
 XX
 PI Hood L, Chaudhary PM;
 XX
 DR WPI: 2001-101569/11.
 XX
 PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal Kinase and apoptosis activities,
 PT for therapeutic purposes
 XX

PS Example 8; Fig 11; 60pp; English.

XX The present sequence is a death effector domain (DED) of a protein
 CC that has been shown to regulate the nuclear factor-kappa
 CC B (NF-kB), Jun N-terminal kinase (JNK) and apoptosis pathways. It
 CC is provided in a specification relating to novel mutants (D73A, L74A and
 CC L75A) for Caspase-8 which are also useful for regulating NF-kB, JNK
 CC and apoptosis activities. The Caspase-8 mutants are useful for
 CC therapeutic purposes and in test methods or assays for determining
 CC whether a candidate compound has a significant effect upon cell
 CC activities, especially NF-kB, JNK and apoptosis, so as to facilitate the
 CC discovery and/or design of therapeutic agents.

XX Sequence 83 AA;

SO Query Match 19.9%; Score 51; DB 22; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.2e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILRRVDPE 131
 DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILRRVDPE 83

RESULT 14

ID ABB81755 standard; protein; 85 AA.

XX ABB81755;

XX 10-SEP-2002 (first entry)

DE Tumour necrosis factor Fas associated death domain death effector domain.

XX Tumour necrosis factor; receptor; TNFR-1; death domain; DED;

KM TNFR-1 DD; Fas associated death domain; FADD; death effector domain;

KM protein co-ordinate data.

XX Unidentified.

OS US2002045578-A1.

PN 18-APR-2002.

XX 14-MAY-2001; 2001US-0854906.

PF 22-MAY-2000; 2000US-206215P.

XX (SUKI/) SUKITS S F.

PA (XUGG/) XU G.

PA (LINL/) LIN L.

PA (TELL/) TELLIEZ J.

PA (HSUS/) HSU S.

XX Sukits SF, Xu G, Lin L, Telliez J, Hsu S;

PI WPI; 2002-443412/47.

DR Solution comprising tumor necrosis factor receptor 1 death domain,
 PT useful for identifying potential inhibitor of tumor necrosis factor
 PT receptor 1 death domain

XX Disclosure; Fig 7; 49pp; English.

XX The sequence represents the tumour necrosis Fas associated death domain
 CC death effector domain (FADD DED). The invention relates to a novel
 CC solution comprising a tumour necrosis factor receptor 1 death domain. The
 CC solution is useful for identifying a potential inhibitor of TNFR-1 DD,
 CC for the design and selection of potent and selective inhibitors of TNF
 CC signalling pathways, and for generating a three-dimensional structure for
 CC an unknown molecule or molecular complex.

XX Sequence 85 AA;

Query Match 19.9%; Score 51; DB 23; Length 85;
 Best Local Similarity 100.0%; Pred. No. 3.3e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILRRVDPE 131
 DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLASLRHRDILRRVDPE 83

RESULT 15

ID AAW76623 standard; protein; 81 AA.

XX AAW76623;

XX 12-JUL-1999 (first entry)

DE Human FADD protein fragment containing death effector domain.

XX Death effector domain; human; murine; anti-apoptotic; treatment;

KM HIV infection; autoimmune disease; FADD protein.

XX Homo sapiens.

OS Key Location/Qualifiers

EH Misc-difference 6

FT /label= unknown

XX DEL9713393-A1.

XX 08-OCT-1998.

XX 01-APR-1997; 97DE-1013393.

XX 01-APR-1997; 97DE-1013393.

PA (TSCH/) TSCHOPP J.

PA (APOT-) APOTTECH SA.

XX Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;

PI Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;

PI Thome M, Tschopp J, Hofmann K;

XX WPI; 1998-532710/46.

DR New DNA encoding for anti-apoptotic gene product - used to treat HIV
 PT infections and autoimmune diseases

XX Disclosure; Fig 2; 45pp; German.

XX This invention describes novel human and mouse anti-apoptotic gene
 CC products which contain at least one death effector domain. The products
 CC of the invention are used in the treatment of HIV infections and
 CC autoimmune diseases.

XX Sequence 81 AA;

SO Query Match 14.5%; Score 37; DB 19; Length 81;
 Best Local Similarity 100.0%; Pred. No. 5.3e-27;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLAS 117
 DB 33 KRRLRVSGGLDFSMLEQNDLEPGHTELLRELLAS 69

Search completed: June 19, 2003, 10:45:32
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:28:30 ; Search time 70 Seconds

(Without alignments)
487.317 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302

Sequence: 1 VNOAPECRFGGCGILGPKR..... RSGAMSPNSMNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1981.DAT:*
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4: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1983.DAT:*
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6: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1992.DAT:*
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21: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1302	100.0	256	18	AAW11894	Modulator of cellu
2	1299	99.8	256	17	AAW11894	MORT-1 modulator o
3	1047	80.4	208	21	AAW51329	Human FADD protein
4	1040	79.9	208	17	AAW03653	FADD (Fas-associat
5	1040	79.9	208	20	AAW96154	Human FADD protein
6	1040	79.9	208	22	AAW84804	Human FADD protein
7	1033	79.3	208	22	AAW61119	Human FADD. Homo
8	1028	79.0	208	20	AAW87493	Amino acid sequenc
9	985.5	75.7	201	20	AAW87492	Amino acid sequenc
10	982.5	75.5	201	20	AAW87491	Amino acid sequenc

11	719.5	55.3	205	22	AAW61900	Mouse apoptosis me
12	401	30.8	83	22	AAW84800	FADD death effecto
13	401	30.8	83	22	AAW61115	Human FADD DED1 do
14	401	30.8	85	23	AAW81755	Tumour necrosis fa
15	375	28.8	81	19	AAW76623	Human FADD protein
16	370.5	28.5	117	22	AAW61902	Mouse apoptosis me
17	349	26.8	88	22	AAW61901	Mouse apoptosis me
18	346	26.6	99	23	AAW81754	Tumour necrosis fa
19	318	24.4	62	17	AAW00210	Human MORT-1 prote
20	125.5	9.6	480	22	AAW06523	Mouse caspase 8 pr
21	122.5	9.4	239	22	AAW62302	Drosophila melanog
22	122	9.4	180	22	AAW84803	Human caspase 8 pr
23	122	9.4	180	22	AAW61118	Human caspase-8.
24	122	9.4	220	19	AAW75961	Human Caspase-8n.
25	122	9.4	235	18	AAW11892	MORT-1 binding pro
26	122	9.4	257	18	AAW31735	Cell death-associat
27	122	9.4	261	18	AAW11898	MACH isoform beta4
28	122	9.4	277	18	AAW11893	MACH isoform beta3
29	122	9.4	464	18	AAW11895	MACH isoform alpha
30	122	9.4	479	18	AAW31523	Interleukin-1 beta
31	122	9.4	479	18	AAW11891	MACH isoform alpha
32	122	9.4	479	19	AAW75963	Human caspase-8.
33	122	9.4	479	22	AAW00605	Human caspase-8 L7
34	117	9.0	479	22	AAW84812	Human caspase-8 L7
35	117	9.0	479	22	AAW84813	Human caspase-8 mu
36	117	9.0	479	22	AAW61127	Human Caspase-8 mu
37	117	9.0	479	22	AAW61128	Human Caspase-8 mu
38	116.5	8.9	291	21	AAW67420	Usurpin-gamma poly
39	116.5	8.9	1975	22	AAW62094	Drosophila melanog
40	116	8.9	81	19	AAW75962	Human Caspase-8L1
41	116	8.9	83	22	AAW84796	Caspase 8 death ef
42	116	8.9	83	22	AAW61111	Human caspase-8 DE
43	116	8.9	110	22	AAW30659	Peptide #3310 enco
44	116	8.9	110	22	AAW35830	Peptide #3336 enco
45	116	8.9	110	22	AAW21245	Protein #3244 enco

ALIGNMENTS

RESULT 1

ID AAW11894 standard; Protein; 256 AA.

AC AAW11894;

XX 29-OCT-1997 (first entry)

XX Modulator of cellular toxicity (MORT-1).

XX MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;

XX antibody; FAS ligand receptor; FAS-R; death domain region; septic shock;

XX tumour necrosis factor; tumour; HIV-1 infection; oligodendrocyte death;

XX apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis;

XX autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;

XX TNF; Therapy.

XX Homo sapiens.

XX MO9703998-AL.

XX 06-FEB-1997.

XX 14-JUN-1996; 96WO-US10521.

XX 16-APR-1996; 96IL-0117932.

XX 17-AUG-1995; 95IL-0114615.

XX 14-SEP-1995; 95IL-0114986.

XX 27-SEP-1995; 95IL-0116588.

XX (WEIN/) WEINMURZEL H.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Boldin M, Goltssev IV, Goncharov T, Wallach D;
 XX
 DR MPI: 1997-132570/12.
 DR N-PSDB: AAT61397.
 XX
 XX New DNA encoding MACH protein that interacts with MORT-1 protein -
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX
 PS Disclosure: Page 102-103; 163pp; English.
 CC
 CC This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAT1892), designated MACH. MORT-1 binds to the FAS ligand receptor.
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p53-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.
 CC
 XX
 SQ Sequence 256 AA:
 Query Match 100.0%; Score 1302; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.8e-125;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNQAECRFGGIIPLGKRRDLARASEPTGARRAGOPPPPLADPAMPDPLVLLHSVS 60
 Db 1 VNQAECRFGGIIPLGKRRDLARASEPTGARRAGOPPPPLADPAMPDPLVLLHSVS 60
 QY 61 SLSSELTETLKFICIGRVYRKRLERVOGDLFSLMLEQNDLEPGHTELLASLR 120
 Db 61 SLSSELTETLKFICIGRVYRKRLERVOGDLFSLMLEQNDLEPGHTELLASLR 120
 QY 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDVGKDWRLARQLKVSDFKIDSIEDR 180
 Db 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDVGKDWRLARQLKVSDFKIDSIEDR 180
 QY 181 YPRNLTERRRESLRIRKTEKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 Db 181 YPRNLTERRRESLRIRKTEKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 QY 241 MSPMSWNSDASTSEAS 256
 Db 241 MSPMSWNSDASTSEAS 256
 RESULT 2
 AAR98346
 ID AAR98346 standard; Protein; 256 AA.
 XX
 AC AAR98346;
 XX
 DT 13-SEP-1996. (first entry)
 XX
 DE MORT-1 modulator of FAS receptor.
 XX
 KW MORT-1, HFL: FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 160..221
 FT /Label= Death domain
 PN WO9618641-A1.
 XX
 XX 20-JUN-1996.
 PD
 XX
 XX 14-DEC-1995; 95WO-US16542.
 PF
 XX 16-JUL-1995; 95IL-0114615.
 PR 15-DEC-1994; 94IL-0112022.
 PR 19-FEB-1995; 95IL-0112692.
 XX
 PA (WEIN/) WEINMUTZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI
 XX
 XX Boldin M, Melt I, Varfolomeev E, Wallach D;
 DR MPI: 1996-100569/30.
 DR N-PSDB: AAT30372.
 XX
 PT MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells
 XX
 PS Claim 5; Fig 4; 72pp; English.
 CC
 CC MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFL,
 CC is a novel protein that binds to the intracellular domain (Fas-IC) of
 CC the Fas ligand receptor Fas-R (or Fas/APOL), and is capable of
 CC modulating the function of Fas-R. MORT-1 is also capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from HeLa cells.
 CC MORT-1 can be used to modulate the Fas-R ligand on cells carrying
 CC an Fas-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.
 CC
 XX
 SQ Sequence 256 AA:
 Query Match 99.8%; Score 1299; DB 17; Length 256;
 Best Local Similarity 99.6%; Pred. No. 5.7e-125;
 Matches 255; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNQAECRFGGIIPLGKRRDLARASEPTGARRAGOPPPPLADPAMPDPLVLLHSVS 60
 Db 1 VNQAECRFGGIIPLGKRRDLARASEPTGARRAGOPPPPLADPAMPDPLVLLHSVS 60
 QY 61 SLSSELTETLKFICIGRVYRKRLERVOGDLFSLMLEQNDLEPGHTELLASLR 120
 Db 61 SLSSELTETLKFICIGRVYRKRLERVOGDLFSLMLEQNDLEPGHTELLASLR 120
 QY 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDVGKDWRLARQLKVSDFKIDSIEDR 180
 Db 121 HDLLRRVDFEAGAAAGAPGEEDICAFNVICDVGKDWRLARQLKVSDFKIDSIEDR 180
 QY 181 YPRNLTERRRESLRIRKTEKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 Db 181 YPRNLTERRRESLRIRKTEKRNATVAHLVGLRSCOMLVADLVOEQARDLONRSGA 240
 QY 241 MSPMSWNSDASTSEAS 256
 Db 241 MSPMSWNSDASTSEAS 256
 RESULT 3
 AAT51329
 ID AAT51329 standard; Protein; 208 AA.
 XX

AC AAY51329;
 XX 19-APR-2000 (first entry)
 XX Human FADD protein.
 DE Human FADD protein.
 XX FADD; human; antisense; inhibitor; Fas-associated death domain.
 XX Homo sapiens.
 OS US6015712-A.
 XX 18-JAN-2000.
 XX 19-JUL-1999; 99US-0357072.
 XX 19-JUL-1999; 99US-0357072.
 XX 19-JUL-1999; 99US-0357072.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cosset LM, Baker BF, Zhang H;
 XX WPI; 2000-126316/11.
 DR N-PSDB; AAZ44745.
 XX Antisense oligonucleotides, useful for inhibiting human Fas-associated
 PT death domain (FADD) expression are targeted to the 3' untranslated
 PT region of the FADD gene -
 XX Example 13; Column 43-46; 37pp; English.
 XX This invention describes novel antisense oligonucleotides (OGNs) (1)
 CC 8-30 nucleotides in length that specifically hybridize with and inhibit
 CC nucleic acids encoding human Fas-associated death domain (FADD).
 CC Targeted to the 3' untranslated region (3'UTR). (1) can be used to treat
 CC animals, especially humans, suspected of having or being prone to a
 CC disease or condition associated with FADD expression. This sequence
 CC represents the human FADD protein described in the method of the
 CC invention.
 CC
 XX Sequence 208 AA;
 SQ
 Query Match 80.4%; Score 1047; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.3e-99;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Human; FADD; Fas-associating protein with novel death domain;
 KW Apoptosis; Fas receptor; death domain; gene therapy; antibody;
 KW Immunossay; drug screening; diagnostic; AIDS; antiinflammatory;
 KW antitumour; cerebroprotective; neuroprotective.
 XX Homo sapiens.
 OS
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 1..125
 FT /note= "N-terminal fragment, inducing apoptosis but
 FT not binding to Fas receptor"
 FT 35..208
 FT /note= "C-terminal active fragment"
 FT 41..208
 FT /note= "C-terminal active fragment"
 FT 42..208
 FT /note= "Fas receptor-binding NFD-2 polypeptide"
 FT 61..208
 FT /note= "Fas receptor-binding NFD-3 polypeptide"
 FT 80..208
 FT /note= "Fas receptor-binding NFD-4 polypeptide"
 FT /note= "Fas receptor-binding NFD-4 polypeptide"
 FT Misc-difference 121
 FT /note= "Altered to Asn in FADDmt mutant"
 FT 111..177
 FT Domain
 FT /note= "Death domain"
 PW W09631603-A2.
 PD 10-OCT-1996.
 XX 28-FEB-1996; 96WO-US02857.
 XX 18-MAY-1995; 95US-0443982.
 PR 03-APR-1995; 95US-0416379.
 XX (UNMI) UNIV MICHIGAN.
 PA Dixit VM, O'Rourke K;
 PI WPI; 1996-465026/46.
 DR N-PSDB; AAT39397.
 XX FADD protein that binds to cytoplasmic region of Fas receptor - for
 PT identifying inhibitors of Fas-associated apoptosis useful for
 PT treating e.g. AIDS, leukaemia, stroke, etc
 PT
 XX Example 1; Fig 2A-B; 96pp; English.
 PS The sequence corresponds to FADD (Fas-associating protein with novel
 CC death domain), which binds the cytoplasmic region of a Fas receptor,
 CC and modulates apoptosis induced by activation of the receptor by
 CC ligand binding. The FADD cDNA has been isolated using a yeast
 CC two-hybrid system to screen for proteins interacting with the Fas
 CC cytoplasmic domain. The protein contains a death domain with
 CC interacts with the death domain of Fas. Mutation of Val-121 to
 CC Asn in mutant FADDmt disrupts binding and/or signalling properties.
 CC C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor
 CC cytoplasmic domain in vitro. An N-terminal fragment induces
 CC apoptosis but does not bind the Fas receptor. The encoding DNA may
 CC be used in gene therapy, and the protein or a corresponding antibody
 CC may be used to screen for agents modulating FADD pathway cellular
 CC functions and Fas-associated apoptosis, for use in therapy of e.g.
 CC AIDS, inflammation, leukaemia, myocardial infarction, degenerative
 CC disease, etc.
 CC
 XX Sequence 208 AA;
 SQ
 Query Match 79.9%; Score 1040; DB 17; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.7e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDPLVLLHSVSSLSSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 60
 QY 109 ELRLRELLASLRHHDLRLRYDDEPAGAAAGAPGEEDLCAAFVNICDNGKMRRLAROLK 168
 Db 61 ELRLRELLASLRHHDLRLRYDDEPAGAAAGAPGEEDLCAAFVNICDNGKMRRLAROLK 120
 QY 169 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKEKATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKEKATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 5
 AAM96154
 ID AAM96154 standard; Protein; 208 AA.
 AC AAM96154;
 DT 27-APR-1999 (first entry)
 DE Human FADD protein.
 KW FIP: FADD interacting protein; FADD: Fas-associated protein with a novel death domain; cell death; apoptosis; Alzheimer's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
 KW amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
 KW protozoa; neoplasia; dysplasia; hyperplasia.
 OS Homo sapiens.
 PN W09900499-A1.
 PD 07-JAN-1999.
 PF 26-JUN-1998; 98MO-US13320.
 PR 03-JUN-1998; 98US-0087886.
 PR 26-JUN-1997; 97US-0050792.
 PA (CHIR) CHIRON CORP.
 PI Chen TT, Williams LT;
 DR WPI; 1999-095745/08.
 DR N-PSDB; AAX08910.
 PT New FADD (Fas-associated protein with a novel death domain)-interacting Protein - useful for inducing or preventing apoptosis in a cell, to aid in controlling apoptosis-related diseases
 PS Disclosure; Page 47; 58pp; English.

An epitope of human FADD (Fas-associated protein with a novel death domain)-interacting protein (FIP protein) comprising amino acids 348-727 of the protein described in AAM96153, can be used to induce or prevent apoptosis in a cell. Specifically, decreasing the levels of FIP348-727 prevents apoptosis. This is useful in cells which are dying prematurely, eg: Alzheimer's disease, Acquired Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic lateral sclerosis (and other muscle wasting diseases), autoimmune diseases, and diseases where cells are infected with a pathogen (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the levels of FIP 348-727 induces apoptosis which is useful in cells suffering from neoplasias, dysplasias, hyperplasias, or their symptoms. Purified and isolated FIP subgenomic polynucleotides are useful as primers to obtain more copies of the nucleotides, and as probes that identify wild-type or mutant coding sequences. They are also useful for expressing FIP mRNA, proteins or fusion proteins, and in the generation of FIP antisense oligonucleotides and

CC ribozymes. They are also useful in expression constructs and in
 CC gene delivery vehicles (optionally in combination with a condensing
 CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
 CC (including variants), FIP-specific ribozymes or single-chain
 CC antibodies into eukaryotic cells. This is the human FADD protein.
 CC Human FIP protein binds to amino acids 1-110 of this sequence.
 SQ Sequence 208 AA:
 Query Match 79.9%; Score 1040; Db 20; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.7e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSLSSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 108
 Db 1 MDPLVLLHSVSSLSSELTFLKFLCIGRVGKRLKERVQSGLDLFSMLLENDLEPGHT 60
 QY 109 ELRLRELLASLRHHDLRLRYDDEPAGAAAGAPGEEDLCAAFVNICDNGKMRRLAROLK 168
 Db 61 ELRLRELLASLRHHDLRLRYDDEPAGAAAGAPGEEDLCAAFVNICDNGKMRRLAROLK 120
 QY 169 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKEKATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTIEDRYPNLTERVRESLRIMKNTKEKATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 6
 AAB84804
 ID AAB84804 standard; Protein; 208 AA.
 AC AAB84804;
 DT 12-JUL-2001 (first entry)
 DE Human FADD prodomain.
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 OS Homo sapiens.
 PN US6207458-B1.
 PD 27-MAR-2001.
 PF 07-MAY-1998; 98US-0074044.
 PR 07-MAY-1998; 98US-0074044.
 PA (UNIT) UNIV WASHINGTON.
 PI Chaudhary PM, Hood L;
 DR WPI; 2001-342087/36.
 PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis activity by comparing cell activity in presence and absence of proteinaceous species having two death effector domain and test compound
 PS Disclosure; Column 51-52; 62pp; English.

The present invention relates to testing candidate compounds to determine whether they affect NF-kappaB, JNK and apoptosis activity. The method involves the use of 2 death effector domains (DED). The compounds identified by the invention have therapeutic applications and are useful for regulating cellular NFkappaB, JNK and apoptosis activity. The assay is useful for identifying pharmacological agents or lead compounds generally involved in assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a prodomain used in the invention.
XX Sequence 208 AA.

Query Match 79.9%; Score 1040; DB 22; Length 208;
Best Local Similarity 99.5%; Pred. No. 1.7e-98;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCICLRVYKRIKLERVQSGIDLSMLEQNDLEPGHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFCICLRVYKRIKLERVQSGIDLSMLEQNDLEPGHT 60
QY 109 ELIRELLASLRRLDLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 168
DB 61 ELIRELLASLRRLDLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 120
QY 169 VSDTKIDSIDRYPNLTERRVRESLRIMKTERENATVAHLVGLSCQNLVADLVQEV 228
DB 121 VSDTKIDSIDRYPNLTERRVRESLRIMKTERENATVAHLVGLSCQNLVADLVQEV 180
QY 229 QQARDLQNRSGAMSPMSWNSDASTSEAS 256
DB 181 QQARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 7
AAB61119
ID AAB61119 standard; protein; 208 AA.

XX AAB61119;

DT 02-MAY-2001 (first entry)

DE Human FADD.

XX Human FADD; apoptotic; nuclear factor-kappa B; NF-kB;

KM Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant.

OS Homo sapiens.

PN US6160095-A.

PD 12-DEC-2000.

PF 24-AUG-1999; 99US-0382155.

PR 07-MAY-1998; 98US-0074044.

PA (UNIT) UNIV WASHINGTON.

PA (STOW-) STOWERS INST MEDICAL RES.

PI Hood L, Chaudhary PM;

DR WPL; 2001-101569/11.

PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating

PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,

PT for therapeutic purposes

PS Example 8; Fig 11; 60pp; English.

XX The present sequence has been shown to regulate the nuclear factor-kappa

CC B (NF-kB), Jun N-terminal kinase (JUNK), and apoptosis pathways. It

CC is provided in a specification relating to novel mutants (D73A, L74A and

CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK

CC and apoptosis activities. The Caspase-8 mutants are useful for

CC therapeutic purposes and in test methods or assays for determining

CC whether a candidate compound has a significant effect upon cell

CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the

CC discovery and/or design of therapeutic agents.

CC Sequence 208 AA;

Query Match 79.3%; Score 1033; DB 22; Length 208;
Best Local Similarity 99.0%; Pred. No. 9.1e-98;
Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCICLRVYKRIKLERVQSGIDLSMLEQNDLEPGHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFCICLRVYKRIKLERVQSGIDLSMLEQNDLEPGHT 60
QY 109 ELIRELLASLRRLDLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 168
DB 61 ELIRELLASLRRLDLRRVDDFEAGAAAGAPGEDICAFNYICDVGKDMRLAROLK 120
QY 169 VSDTKIDSIDRYPNLTERRVRESLRIMKTERENATVAHLVGLSCQNLVADLVQEV 228
DB 121 VSDTKIDSIDRYPNLTERRVRESLRIMKTERENATVAHLVGLSCQNLVADLVQEV 180
QY 229 QQARDLQNRSGAMSPMSWNSDASTSEAS 256
DB 181 QQARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 8
AAM87493
ID AAM87493 standard; protein; 208 AA.

XX AAM87493;

DT 12-FEB-1999 (first entry)

DE Amino acid sequence of MORT1 isoform MORT1G173A from human brain.

XX MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/AP01;

KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;

KM in vivo agent; neuronal apoptosis; human.

OS Homo sapiens.

PN WO9849297-A1.

PD 05-NOV-1998.

PF 14-APR-1998; 98WO-US07439.

PR 25-APR-1997; 97US-0044835.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Blingham BW, Birsan C, Wood AT, Young KH;

DR WPL; 1999-009424/01.

PT Human, neuronal MORT1 isoform(s) - used as screening agents in

PT diagnosing CNS diseases, and in discovering CNS-specific

PT anti-apoptotic compounds

PS Claim 7; Pages 30-31; 31pp; English.

XX This represents the amino acid sequence of a MORT1 isoform MORT1G173A.

CC The encoding cDNA was isolated from human brain and deposited under the

CC accession number ATCC 209019. The cDNA has a nucleotide substitution (G

CC to A) at basepair position 173 of the published MORT1 coding sequence.

CC The invention relates to three MORT1 nucleic acid isoforms (AAV71928 to

CC AAV71930) that encode proteins which can interact with the death domain

CC of Fas/AP01. The MORT1 isoforms can also interact with MACH alpha1 or

CC other members of the ICE/Ced3 (Caspase) family of proteins. The

CC transcript isoforms, together with their encoded proteins are useful as

CC screening agents in diagnosing CNS diseases, and in discovering

CC CNS-specific anti-apoptotic compounds. They are useful in gene therapy

CC either as in vivo agents in humans or as experimental tools in

CC manipulating neuronal apoptosis in cell culture and animal model

CC systems.

SO Sequence 208 AA; 79.0%; Score 1028; DB 20; Length 208;
 Query Match 98.6%; Pred. No. 3e-97;
 Best Local Similarity 98.6%; Pred. No. 3e-97;
 Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSSSSELTELFKLCGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108
 |||||
 DB 1 MDPFLVLLHSVSSSSSELTELFKLCGRVYKRLERVOGSLDFSMLEQNDLEPGHT 60
 |||||

QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFNVICDNGKMRRLAROLK 168
 |||||

DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFNVICDNGKMRRLAROLK 120
 |||||

QY 169 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
 |||||

DB 121 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGALRSCOMNLVADLVQEV 180
 |||||

QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
 |||||

DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208
 |||||

RESULT 9
 AAM87492
 ID AAM87492 standard; Protein; 201 AA.
 AC AAM87492;
 XX
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of MOR1L isoform MOR1del121 from human brain.
 XX
 KM MOR1L; MOR1del121; NTERA2; CNS; Isoform; death domain; Fas/AP01;
 KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KM In vivo agent; neuronal apoptosis; human.
 XX
 OS Homo sapiens.
 XX
 PM W09849297-A1.
 XX
 PD 05-NOV-1998.
 XX
 PE 14-APR-1998; 98WO-US07439.
 XX
 PF 25-APR-1997; 97US-0044835.
 XX
 PR (AMHP) AMERICAN HOME PROD CORP.
 XX
 PA Blingham BW, Birsan C, Wood AT, Young KH;
 XX
 PI WPI: 1999-009424/01.
 XX
 DR N-PSDB; AAV71929.
 XX
 PT Human, neuronal MOR1L isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX
 PS Claim 6; Pages 28-29; 31pp; English.
 XX
 CC This represents the amino acid sequence of a MOR1L isoform MOR1del121.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209018. The cDNA has a 21 base pair deletion as
 CC compared to the published MOR1L sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MOR1L nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/AP01. The MOR1L isoforms can also interact with the
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model

CC systems.
 XX
 SO Sequence 201 AA; 75.7%; Score 985.5; DB 20; Length 201;
 Query Match 95.7%; Pred. No. 6.6e-93;
 Best Local Similarity 95.7%; Pred. No. 6.6e-93;
 Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPFLVLLHSVSSSSSELTELFKLCGRVYKRLERVOGSLDFSMLEQNDLEPGHT 108
 |||||
 DB 1 MDPFLVLLHSVSSSSSELTELFKLCGRVYKRLERVOGSLDFSMLEQNDLEPGHT 57
 |||||

QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFNVICDNGKMRRLAROLK 168
 |||||

DB 58 ---ELRLASLRHDLRRVDFEAGAAAGAAAGPEEDLCAAFNVICDNGKMRRLAROLK 113
 |||||

QY 169 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
 |||||

DB 114 VSDTRKIDIEDRPNTLTERVRESLRINKTEKENATVAHLVGALRSCOMNLVADLVQEV 173
 |||||

QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
 |||||

DB 174 QOARDLQNRSGAMSPMNSNDASTSEAS 201
 |||||

RESULT 10
 AAM87491
 ID AAM87491 standard; Protein; 201 AA.
 AC AAM87491;
 XX
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of MOR1L isoform MOR1del121 from NTERA2 cells.
 XX
 KM MOR1L; MOR1del121; NTERA2; CNS; Isoform; death domain; Fas/AP01;
 KM MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KM In vivo agent; neuronal apoptosis; human.
 XX
 OS Homo sapiens.
 XX
 PM W09849297-A1.
 XX
 PD 05-NOV-1998.
 XX
 PE 14-APR-1998; 98WO-US07439.
 XX
 PF 25-APR-1997; 97US-0044835.
 XX
 PR (AMHP) AMERICAN HOME PROD CORP.
 XX
 PA Blingham BW, Birsan C, Wood AT, Young KH;
 XX
 PI WPI: 1999-009424/01.
 XX
 DR N-PSDB; AAV71928.
 XX
 PT Human, neuronal MOR1L isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX
 PS Claim 5; Pages 26-27; 31pp; English.
 XX
 CC This represents the amino acid sequence of a MOR1L isoform MOR1del121.
 CC The encoding cDNA was isolated from NTERA2 cells and deposited under the
 CC accession number ATCC 209013. The cDNA has a 21 base pair deletion as
 CC compared to the published MOR1L sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MOR1L nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/AP01. The MOR1L isoforms can also interact with the
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy

CC either as in vivo agents in humans or as experimental tools in
CC manipulating neuronal apoptosis in cell culture and animal model
CC systems.

SO Sequence 201 AA;

Query Match 75.5%; Score 982.5; DB 20; Length 201;
Best Local Similarity 95.7%; Pred. No. 1.3e-92;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

OY 49 MDPLVYLHSVSSSSSELTEKFLCIGRVYRKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPLVYLHSVSSSSSELTEKFLCIGRVYRKRLERVOGSLDFSMLEQNDLEPGHT 57

OY 109 ELRLLELASLRHDLRRVDFEAGAAAGAPGEEDLCANFNVICDNYGKDMRLAROLK 168

DB 58 ----ELRLLELASLRHDLRRVDFEAGAAAGAPGEEDLCANFNVICDNYGKDMRLAROLK 113

OY 169 VSDPKRISIEDRYPRNLTFRERRESLRKNTKEKENATVAHLVGLRSCOMNLVADLYGEV 228

DB 114 VSDPKRISIEDRYPRNLTFRERRESLRKNTKEKENATVAHLVGLRSCOMNLVADLYGEV 173

OY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256

DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 11

ID AAB61900 standard; Protein; 205 AA.

XX AAB61900;

DT 08-MAY-2001 (first entry)

DE Mouse apoptosis mediator FADD.

KM FADD; DED; FADD-DED; death effector domain; apoptosis mediator;

KM bacterial; cell death; reactive oxygen species; ROS; mouse.

OS Mus sp.

PN WO200104153-A1.

PD 18-JAN-2001.

PF 11-JUL-2000; 2000WO-KR00721.

PR 12-JUL-1999; 99KR-0027964.

PA (IMAGE-) IMAGEGENE CO LTD.

PI Kim S, Kim K.

DR WPI: 2001-138318/14.

DR N-PSDB: AAC85064.

PT Novel death effector domain of mammalian apoptosis mediator, for

PT inducing bacterial and mammalian cell death by enhancing cellular level

PT of reactive oxygen species -

PS Claim 1; Page 43-44; 47pp; English.

CC The invention relates to a death effector domain (DED) of a mammalian

CC apoptosis mediator (FADD). The FADD-DED induces bacterial and mammalian

CC cell death by enhancing cellular level of reactive oxygen species (ROS).

CC The present sequence represents a mouse FADD, a pro-apoptotic mediator

CC consisting of N-terminal death effector domain (DED) and C-terminal death

Best Local Similarity 68.4%; Pred. No. 1.4e-65;

Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

OY 49 MDPLVYLHSVSSSSSELTEKFLCIGRVYRKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPLVYLHSVSSSSSELTEKFLCIGRVYRKRLERVOGSLDFSMLEQNDLEPGHT 60

OY 109 ELRLLELASLRHDLRRVDFEAGAAAGAPGEEDLCANFNVICDNYGKDMRLAROLK 168

DB 61 ELRLLELASLRHDLRRVDFEAGAAAGAPGEEDLCANFNVICDNYGKDMRLAROLK 120

OY 169 VSDPKRISIEDRYPRNLTFRERRESLRKNTKEKENATVAHLVGLRSCOMNLVADLYGEV 228

DB 121 VSEAKMDIEREYPRSLSERRESLRKNTKEKENATVAHLVGLRSCOMNLVADLYGEV 180

OY 229 QOARDLQNRSGAMSPMNSDASTSE 254

DB 181 QES--VSEKEMSPVLRDSTVSSSE 203

RESULT 12

ID AAB84800 standard; Protein; 83 AA.

XX AAB84800;

DT 12-JUL-2001 (first entry)

DE FADD death effector domain 1.

KM NF-kappaB; JNK; apoptosis; death effector domain; DED.

OS Homo sapiens.

PN US6207458-B1.

PD 27-MAR-2001.

PF 07-MAY-1996; 98US-0074044.

PR 07-MAY-1996; 98US-0074044.

PA (UNIT) UNIV WASHINGTON.

PI Chaudhary PM, Hood L;

DR WPI: 2001-342087/36.

PT Testing candidate compound affecting cellular NFkappaB JNK, apoptosis

PT activity by comparing cell activity in presence and absence of

PT proteinaceous species having two death effector domain and test

PT compound

PS Claim 10; Column 45-47; 62pp; English.

CC The present invention relates to testing candidate compounds to

CC determine whether they affect NF-kappaB, JNK and apoptosis activity.

CC The method involves the use of 2 death effector domains (DED). The

CC compounds identified by the invention have therapeutic

CC applications and are useful for regulating cellular NFkappaB, JNK

CC and apoptosis activity. The assay is useful for identifying

CC pharmacological agents or lead compounds generally involved in

CC assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a death effector domain of the invention.

SO Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 2.2e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 49 MDPLVYLHSVSSSSSELTEKFLCIGRVYRKRLERVOGSLDFSMLEQNDLEPGHT 108

DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSLDIFSMLLEQNDLEPGHT 60
 QY 109 ELRLRLASLRHDLRRVDFE 131
 DB 61 ELRLRLASLRHDLRRVDFE 83

RESULT 13
 AAB61115
 ID AAB61115 standard; protein; 83 AA.

AC AAB61115;

DT 02-MAY-2001 (first entry)

DE Human FADD DED1 domain.

KM Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KW Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant;
 KM death effector domain; DED.

OS Homo sapiens.

PN US6160095-A.

PD 12-DEC-2000.

PF 24-AUG-1999; 990US-0382155.

PR 07-MAY-1998; 980US-0074044.

PA (UNIM) UNIV WASHINGTON.
 (STOW) STOWERS INST MEDICAL RES.

PI Hood L, Chaudhary PM;

PI WPI; 2001-101569/11.

DR Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PI nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
 PT for therapeutic purposes

PS Example 8; Fig 11; 60pp; English.

XX The present sequence is a death effector domain (DED) of a protein
 CC that has been shown to regulate the nuclear factor-kappa
 CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
 CC is provided in a specification relating to novel mutants (D73A, L74A and
 CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
 CC and apoptosis activities. The Caspase-8 mutants are useful for
 CC therapeutic purposes and in test methods or assays for determining
 CC whether a candidate compound has a significant effect upon cell
 CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
 CC discovery and/or design of therapeutic agents.

CC Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
 Best Local Similarity 98.8%; Pred. No. 2.2e-33;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSLDIFSMLLEQNDLEPGHT 108
 DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSLDIFSMLLEQNDLEPGHT 60

QY 109 ELRLRLASLRHDLRRVDFE 131
 DB 61 ELRLRLASLRHDLRRVDFE 83

RESULT 14
 ABB81755
 ID ABB81755 standard; protein; 85 AA.

XX ABB81755;

DT 10-SEP-2002 (first entry)

DE Tumour necrosis factor Fas associated death domain death effector domain.
 KW Tumour necrosis factor; receptor; TNFR-1; death domain; DED;
 KW TNFR-1 DD; Fas associated death domain; FADD; death effector domain;
 KW protein co-ordinate data.

OS Unidentified.

PN US2002045578-A1.

PD 18-APR-2002.

PF 14-MAY-2001; 2001US-0854906.

PR 22-MAY-2000; 2000US-206215P.

PA (SUKI) SUKITS S F.
 (XUGG) XU G.
 (LINL) LIN L.
 (TELL) TELLIEZ J.
 (HSU) HSU S.

PI Sukits SF, Xu G, Lin L, Telliez J, Hsu S;
 WPI; 2002-443412/47.

DR Solution comprising tumor necrosis factor receptor 1 death domain,
 PT useful for identifying potential inhibitor of tumor necrosis factor
 PT receptor 1 death domain

PS Disclosure; Fig 7; 49pp; English.

XX The sequence represents the tumour necrosis Fas associated death domain
 CC death effector domain (FADD DED). The invention relates to a novel
 CC solution comprising a tumour necrosis factor receptor 1 death domain. The
 CC solution is useful for identifying a potential inhibitor of TNFR-1 DD,
 CC for the design and selection of potent and selective inhibitors of TNF
 CC signalling pathways, and for generating a three-dimensional structure for
 CC an unknown molecule or molecular complex.

CC Sequence 85 AA;

Query Match 30.8%; Score 401; DB 23; Length 85;
 Best Local Similarity 98.8%; Pred. No. 2.2e-33;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSLDIFSMLLEQNDLEPGHT 108
 DB 1 MDPFLVLLHSVSSLSSELTETKFLCIGRVGKRLERVQSLDIFSMLLEQNDLEPGHT 60

QY 109 ELRLRLASLRHDLRRVDFE 131
 DB 61 ELRLRLASLRHDLRRVDFE 83

RESULT 15
 AAW76623
 ID AAW76623 standard; protein; 81 AA.

AC AAW76623;

DT 12-JUL-1999 (first entry)

DE Human FADD protein fragment containing death effector domain.
 KW Death effector domain; human; murine; anti-apoptotic; treatment;
 KW HIV infection; autoimmune disease; FADD protein.

OS	Homo sapiens.
XX	
FH.	Key Location/Qualifiers
FT	Misc-difference 6 /label= unknown
FT	
XX	
PN	DE19713393-A1.
XX	
PD	08-OCT-1998.
XX	
PE	01-APR-1997; 97DE-1013393.
XX	
PR	01-APR-1997; 97DE-1013393.
XX	
PA	(TSCG/) TSCHOFF J. (APOT-) APOTECH SA.
XX	
PI	Bodmer J., Burns K., French EL., Hahne M., Hoffmann K; Pirler M., Raimoldi D., Schneider P., Schroeder M., Steiner V; Thome M., Tschoep U., Hofmann K;
PI	
XX	WPI; 1998-532710/46.
DR	
XX	
PT	New DNA encoding for anti-apoptotic gene product - used to treat HIV infections and autoimmune diseases
XX	
PS	Disclosure; Fig 2; 45pp; German.
CC	
CC	This invention describes novel human and mouse anti-apoptotic gene products which contain at least one death effector domain. The products of the invention are used in the treatment of HIV infections and autoimmune diseases.
CC	
XX	
SQ	Sequence 81 AA:
Query Match	28.8%; Score 375; DB 19; Length 81;
Best Local Similarity	95.1%; Pred. No. 9.8e-31;
Matches 77; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
OY	49 MDPLVLVLSHVSSSLSSSELTREKFLCLGRVVKRLERVOGLDFSMLEONDLPGHT 108 1 MDPSLTLHSVSSSLSSSELTEKFLCLGRVGKRKLEROGLDLSMILEONDLPGHT 60
DB	109 ELLRELLASIRRHDLRRVD 129
OY	61 ELLRELLASIRRHDLRRVD 81
DB	

Search completed: June 19, 2003, 10:36:45
Job time : 71 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:35:30 ; Search time 14 Seconds
(Without alignments)
538,019 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNAPPCRCRFGGILGPKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop: 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/Backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	US-08-983-502-2	Sequence 2, Appl
2	1302	100.0	256	PCT-US95-16542-2	Sequence 2, Appl
3	1302	100.0	256	PCT-US96-10521-2	Sequence 2, Appl
4	1047	80.4	208	US-08-618-164-3	Sequence 3, Appl
5	1040	79.9	208	US-09-074-044A-19	Sequence 19, Appl
6	1033	79.3	208	US-09-382-155-19	Sequence 19, Appl
7	1028	79.0	208	US-09-064-414-6	Sequence 6, Appl
8	985.5	75.7	201	US-09-064-414-4	Sequence 4, Appl
9	982.5	75.5	201	US-09-064-414-2	Sequence 2, Appl
10	436	33.6	85	US-09-042-785A-28	Sequence 28, Appl
11	405	31.1	84	US-08-665-220-64	Sequence 64, Appl
12	405	31.1	84	US-09-291-692-64	Sequence 64, Appl
13	401	30.8	83	US-09-382-155-15	Sequence 15, Appl
14	401	30.8	83	US-09-074-044A-15	Sequence 15, Appl
15	382	29.3	74	US-08-995-159-5	Sequence 5, Appl
16	382	29.3	74	US-08-828-683A-25	Sequence 25, Appl
17	318	24.4	62	US-08-894-626-5	Sequence 5, Appl
18	128.5	9.9	250	US-09-187-789-48	Sequence 48, Appl
19	128.5	9.9	250	US-09-139-600-43	Sequence 43, Appl
20	122	9.4	180	US-09-382-155-18	Sequence 18, Appl
21	122	9.4	180	US-09-074-044A-18	Sequence 18, Appl
22	122	9.4	220	US-08-807-200-2	Sequence 2, Appl
23	122	9.4	220	US-09-001-777-2	Sequence 2, Appl
24	122	9.4	235	US-08-983-502-5	Sequence 5, Appl
25	122	9.4	235	PCT-US96-10521-5	Sequence 5, Appl
26	122	9.4	257	US-08-618-164-2	Sequence 2, Appl
27	122	9.4	261	US-08-983-502-25	Sequence 25, Appl

28	122	9.4	261	5	PCT-US96-10521-25	Sequence 25, Appl
29	122	9.4	277	4	US-08-983-502-8	Sequence 8, Appl
30	122	9.4	277	5	PCT-US96-10521-8	Sequence 8, Appl
31	122	9.4	464	4	US-08-983-502-18	Sequence 18, Appl
32	122	9.4	464	5	PCT-US96-10521-18	Sequence 18, Appl
33	122	9.4	479	2	US-08-807-200-12	Sequence 12, Appl
34	122	9.4	479	3	US-08-852-782-3	Sequence 3, Appl
35	122	9.4	479	4	US-09-001-777-12	Sequence 12, Appl
36	122	9.4	479	4	US-08-983-502-7	Sequence 7, Appl
37	122	9.4	479	5	PCT-US96-10521-7	Sequence 7, Appl
38	119	9.1	709	1	US-08-444-005-17	Sequence 17, Appl
39	117	9.0	75	4	US-09-291-692-66	Sequence 66, Appl
40	117	9.0	479	4	US-09-382-155-27	Sequence 27, Appl
41	117	9.0	479	4	US-09-382-155-28	Sequence 28, Appl
42	117	9.0	479	4	US-09-074-044A-27	Sequence 27, Appl
43	117	9.0	479	4	US-09-074-044A-28	Sequence 28, Appl
44	116	8.9	75	1	US-08-665-220-66	Sequence 66, Appl
45	116	8.9	81	2	US-08-807-200-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-983-502-2
Sequence 2, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yuri V. GOLDBEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-2

Query Match 100.0%; Score 1302; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPECRGGGILPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
DB 1 VNQAPECRGGGILPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
QY 61 SLSSESELTELKFLCGRVYKRRLEKRVQSGDLFSMLEQNDLEPGHTELLRELLASLR 120
DB 61 SLSSESELTELKFLCGRVYKRRLEKRVQSGDLFSMLEQNDLEPGHTELLRELLASLR 120
QY 121 HOLLRVDFEAGAAAGAPGEEDCAAFNVICDNVGMKWRRLARQLKVSDFKIDSIER 180
DB 121 HOLLRVDFEAGAAAGAPGEEDCAAFNVICDNVGMKWRRLARQLKVSDFKIDSIER 180
QY 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCOMLVADLVOEQOARDLONRSGA 240
DB 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCOMLVADLVOEQOARDLONRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 2

PCT-US95-16542-2

Sequence 2, Application PC/TUS9516542

GENERAL INFORMATION:

APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.

APPLICANT: WEINMURZEL, Henry

APPLICANT: WALLACH, David

APPLICANT: BOLDIN, Mark

APPLICANT: VAFIOLOMEV, Eugene

APPLICANT: METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16542

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 112022

FILING DATE: 15-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 112692

FILING DATE: 19-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114615

FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25, 618
REFERENCE/DOCKET NUMBER: WALLACH-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16542-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPECRGGGILPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
DB 1 VNQAPECRGGGILPLGKRRDLARASEPRTGARRAGQPPPLADPANDPFLVLLHSVS 60
QY 61 SLSSESELTELKFLCGRVYKRRLEKRVQSGDLFSMLEQNDLEPGHTELLRELLASLR 120
DB 61 SLSSESELTELKFLCGRVYKRRLEKRVQSGDLFSMLEQNDLEPGHTELLRELLASLR 120
QY 121 HOLLRVDFEAGAAAGAPGEEDCAAFNVICDNVGMKWRRLARQLKVSDFKIDSIER 180
DB 121 HOLLRVDFEAGAAAGAPGEEDCAAFNVICDNVGMKWRRLARQLKVSDFKIDSIER 180
QY 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCOMLVADLVOEQOARDLONRSGA 240
DB 181 YPRNLTERRRESLRIMKTEKENATVAHLVGLRSCOMLVADLVOEQOARDLONRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
DB 241 MSPMSWNSDASTSEAS 256

RESULT 3

PCT-US96-10521-2

Sequence 2, Application PC/TUS9610521

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115, 319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116, 588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117, 932

FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 6,5e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNQAPECFGGGIIIGPLKRDILARASPRREGARRAGCPORPLADPMDFVLLHSYS 60
DB 1 VNQAPECFGGGIIIGPLKRDILARASPRREGARRAGCPORPLADPMDFVLLHSYS 60
QY 61 SLSSELTETKFLCIGRVYRKLEKRVOSGLDLSMLEQNDLPGHTELLRELLASLR 120
DB 61 SLSSELTETKFLCIGRVYRKLEKRVOSGLDLSMLEQNDLPGHTELLRELLASLR 120
QY 121 HDLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRRLAROLKVSPTKIDSIEDR 180
DB 121 HDLLRRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRRLAROLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEVQOARDLQNRGA 240
DB 181 YPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEVQOARDLQNRGA 240
QY 241 MSPMWSNDASTSEAS 256
DB 241 MSPMWSNDASTSEAS 256

RESULT 4

US-08-618-164-3
Sequence 3, Application US/08618164
Patent No. 5712115

GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Braxton, Scott Michael
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,164
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0058 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0195
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 791038
US-08-618-164-3

Query Match 80.4%; Score 1047; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 1,2e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPLVLLHSYSSSSSELTEKFLCIGRVYRKLEKRVOSGLDLSMLEQNDLPGHTE 108
DB 1 MDPLVLLHSYSSSSSELTEKFLCIGRVYRKLEKRVOSGLDLSMLEQNDLPGHTE 108
QY 109 ELLEELLASLRHDLIRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELLEELLASLRHDLIRVDFEAGAAAGAPGEDLCAAFNVICDNGKDMRRLAROLK 120
QY 169 VSDTKIDSIEDRYPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
DB 121 VSDTKIDSIEDRYPRNLTERVRESLIRKTEKENATVAHLVGLRSCOMNLVADLVQEV 180
QY 229 QOARDLQNRGAMSPMWSNDASTSEAS 256
DB 181 QOARDLQNRGAMSPMWSNDASTSEAS 208

RESULT 5

US-09-074-044A-19
Sequence 19, Application US/09074044A
Patent No. 6207458

GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9057
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-19

Query Match 79.9%; Score 1040; DB 4; Length 208;
Best Local Similarity 99.5%; Pred. No. 6.8e-104;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60

QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120

QY 169 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 228
DB 121 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 180

QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 6

US-09-382-155-19
Sequence 19, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 19
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-19

Query Match

79.3%; Score 1033; DB 4; Length 208;
Best Local Similarity 99.0%; Pred. No. 3.9e-103;
Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60

QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120

QY 169 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 228
DB 121 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 180

QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 7

US-09-064-414-6
Sequence 6, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: WOOD, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia

TITLE OF INVENTION: Neuronal MOR1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-4117
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-064-414-6

Query Match

79.0%; Score 1028; DB 4; Length 208;
Best Local Similarity 98.6%; Pred. No. 1.3e-102;
Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSHVSSTLSSELTETKFLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60

QY 109 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 168
DB 61 ELRLRLASLRHDLRRVDFEAGAAAGAEEDLCAAFNVICDNGKDMRRLAROLK 120

QY 169 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 228
DB 121 VSDTKIDSIDERYPNLTERVRESLRINKTEKENATVAHLVGALRSQCNLVADLYOEY 180

QY 229 QOARDLQNRSGAMSPMNSNDASTSEAS 256
DB 181 QOARDLQNRSGAMSPMNSNDASTSEAS 208

RESULT 8

US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: WOOD, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal MOR1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 75.7%; Score 985.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 4.7e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPLVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLQNDLEPHT 108
DB 1 MDPLVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLQNDLEPHT 57
QY 109 ELRLSLRRHDLRRVDDFEAGAAGAAPGEEDLCAAFNVICDNYGKMRRLAROLK 168
DB 58 ----ELASLRHDLRRVDDFEAGAAGAAPGEEDLCAAFNVICDNYGKMRRLAROLK 113
QY 169 VSDTKRDISIEDRPNTLTERVRESLRINKTEKENATVAHLVGAALRSQNNLVADLVQEV 228
DB 114 VSDTKRDISIEDRPNTLTERVRESLRINKTEKENATVAHLVGAALRSQNNLVADLVQEV 173
QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 9
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Bitzan, Camella
TITLE OF INVENTION: Neuronal MORT1 Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany,
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-2

Query Match 75.5%; Score 982.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 9.8e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPLVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLQNDLEPHT 108
DB 1 MDPLVLLHSVSSSSSELTELKFLCGRVYKRLERVOGSLDLSMLLQNDLEPHT 57
QY 109 ELRLSLRRHDLRRVDDFEAGAAGAAPGEEDLCAAFNVICDNYGKMRRLAROLK 168
DB 58 ----ELASLRHDLRRVDDFEAGAAGAAPGEEDLCAAFNVICDNYGKMRRLAROLK 113
QY 169 VSDTKRDISIEDRPNTLTERVRESLRINKTEKENATVAHLVGAALRSQNNLVADLVQEV 228
DB 114 VSDTKRDISIEDRPNTLTERVRESLRINKTEKENATVAHLVGAALRSQNNLVADLVQEV 173
QY 229 QOARDLQNRSGAMSPMNSDASTSEAS 256
DB 174 QOARDLQNRSGAMSPMNSDASTSEAS 201

RESULT 10
US-09-042-785A-28
Sequence 28, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-28

Query Match 33.6%; Score 438; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 9.1e-40;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 LCAAFNYICDVGWDRRLAQLVSPDKISIDRYRNTERYRESLRITKTEKNA 204
DB 1 LCAAFNYICDVGWDRRLAQLVSPDKISIDRYRNTERYRESLRITKTEKNA 60
OY 205 TVALVGLRSCQNNLVADLVQEVQ 229
DB 61 TVALVGLRSCQNNLVADLVQEVQ 85

RESULT 11
US-08-665-220-64
Sequence 64, Application US/08665220
Patent No. 5786173

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,220
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/618,408
FILING DATE: 19-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2165.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "human FADD"
US-08-665-220-64

Query Match 31.1%; Score 405; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 3.2e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 49 MDPLVLLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPLVLLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108

DB 1 MDPLVLLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60
OY 109 ELRELLEASLRHHDLRRVDDFEA 132
DB 61 ELRELLEASLRHHDLRRVDDFEA 84

RESULT 12
US-09-291-692-64
Sequence 64, Application US/09291692
Patent No. 6287795

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Christensen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "human FADD"
US-09-291-692-64

Query Match 31.1%; Score 405; DB 4; Length 84;
Best Local Similarity 98.8%; Pred. No. 3.2e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 49 MDPLVLLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MDPLVLLHSVSSLSSELTFLKLCGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
OY 109 ELRELLEASLRHHDLRRVDDFEA 132
DB 61 ELRELLEASLRHHDLRRVDDFEA 84

RESULT 13
US-09-382-155-15
Sequence 15, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:

APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 83
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 8.3e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCIGRYVKRLERVOGDLFSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFCIGRYVKRLERVOGDLFSMLLEQNDLEPGHT 60
QY 109 ELRELLASLRHDLRRVDDE 131
DB 61 ELRELLASLRHDLRRVDDE 83

RESULT 14
US-09-074-044A-15
Sequence 15, Application US/09074044A
Patent No. 6207458
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MISSOURI
COUNTRY: USA
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-09-074-044A-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 8.3e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFCIGRYVKRLERVOGDLFSMLLEQNDLEPGHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFCIGRYVKRLERVOGDLFSMLLEQNDLEPGHT 60
QY 109 ELRELLASLRHDLRRVDDE 131
DB 61 ELRELLASLRHDLRRVDDE 83

RESULT 15
US-08-995-159-5
Sequence 5, Application US/08995159
Patent No. 6130079
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,159
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488,0860001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-995-159-5

Query Match 29.3%; Score 382; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 7.8e-34;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGKDMRLAROLKYSDFIKDSIEDRYPRNLTERVRESLRINKTEKENATVAHLVG 211
DB 1 ICDNVGKDMRLAROLKYSDFIKDSIEDRYPRNLTERVRESLRINKTEKENATVAHLVG 60
QY 212 ALRSCOMLVADLV 225
DB 61 ALRSCOMLVADLV 74

Thu Jun 19 11:26:31 2003

Search completed: June 19, 2003, 10:39:27
Job time : 15 secs

us-09-933-814-2_1.ra1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:38:50 ; Search time 48 Seconds
(without alignments)
577.103 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNQAPRCFRGGILGPIGRK.....RSGAMSMNNSDASTSEAS 256

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications MA:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	10 US-09-933-814-2	Sequence 2, Appl
2	1302	100.0	256	10 US-09-824-134-2	Sequence 2, Appl
3	405	31.1	84	10 US-09-952-768-64	Sequence 64, Appl
4	390	30.0	81	10 US-09-410-194-9	Sequence 9, Appl
5	386	29.6	82	9 US-10-001-254-39	Sequence 39, Appl
6	382	29.3	74	9 US-10-112-793-25	Sequence 25, Appl
7	382	29.3	74	9 US-10-287-559-5	Sequence 5, Appl
8	369	28.3	77	9 US-10-001-254-35	Sequence 35, Appl
9	318	24.4	62	12 US-10-035-408-5	Sequence 5, Appl
10	128.5	9.9	250	10 US-10-068-564-48	Sequence 48, Appl
11	128.5	9.9	250	10 US-09-989-903-48	Sequence 48, Appl
12	122	9.4	177	10 US-09-410-194-7	Sequence 7, Appl
13	122	9.4	478	9 US-09-009-893-3	Sequence 3, Appl
14	122	9.4	479	10 US-09-410-194-20	Sequence 20, Appl
15	117	9.0	75	10 US-09-952-768-66	Sequence 66, Appl
16	116	8.9	75	9 US-10-001-254-31	Sequence 31, Appl
17	116	8.9	110	10 US-09-864-761-36543	Sequence 36543, A
18	116	8.9	476	10 US-09-954-697-27	Sequence 27, Appl
19	116	8.9	496	10 US-09-952-768-4	Sequence 4, Appl

20	115.5	8.9	656	10 US-09-862-027-30	Sequence 30, Appl
21	111.5	8.6	77	9 US-10-287-559-7	Sequence 7, Appl
22	111.5	8.6	671	9 US-09-981-357A-16	Sequence 16, Appl
23	111.5	8.6	671	10 US-09-758-003-2	Sequence 2, Appl
24	111.5	8.6	671	10 US-09-862-027-29	Sequence 29, Appl
25	110	8.4	221	10 US-09-410-194-15	Sequence 15, Appl
26	110	8.4	221	10 US-09-410-194-22	Sequence 22, Appl
27	110	8.4	480	9 US-09-009-893-2	Sequence 2, Appl
28	110	8.4	480	10 US-09-861-270-2	Sequence 2, Appl
29	110	8.4	480	10 US-09-410-194-11	Sequence 11, Appl
30	110	8.4	480	10 US-09-410-194-17	Sequence 17, Appl
31	108.5	8.3	77	9 US-10-112-793-27	Sequence 27, Appl
32	108	8.3	79	9 US-09-952-768-65	Sequence 65, Appl
33	108	8.3	170	10 US-09-410-194-8	Sequence 8, Appl
34	108	8.3	479	9 US-09-009-893-3	Sequence 4, Appl
35	108	8.3	479	10 US-09-952-768-2	Sequence 2, Appl
36	108	8.3	479	10 US-09-954-697-33	Sequence 33, Appl
37	108	8.3	521	10 US-09-962-834A-2	Sequence 2, Appl
38	108	8.3	571	10 US-09-410-194-21	Sequence 21, Appl
39	106	8.1	77	9 US-10-001-254-33	Sequence 33, Appl
40	92.5	7.1	909	9 US-09-925-299-988	Sequence 988, App
41	92.5	7.1	298	10 US-09-925-299-988	Sequence 988, App
42	92	7.1	298	10 US-09-801-368-230	Sequence 27, App
43	91.5	7.0	832	10 US-09-834-765-2	Sequence 2, Appl
44	91	7.0	2743	9 US-10-037-182-36	Sequence 36, Appl
45	91	7.0	3695	9 US-10-037-182-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1	US-09-933-814-2	Sequence 2, Appl
Patent No.	US20020058798A1	Sequence 2, Appl
GENERAL INFORMATION:		
APPLICANT:	WALLACH, David	
APPLICANT:	BOLDIN, Mark	
APPLICANT:	VARFOLOMEY, Eugene	
APPLICANT:	METZ, Igor	
TITLE OF INVENTION:	MODULATORS OF THE FUNCTION OF FAS/ABOI RECEPTORS	
FILE REFERENCE:	WALLACH-16B	
CURRENT APPLICATION NUMBER:	US/09/933,814	
CURRENT FILING DATE:	2001-08-22	
PRIOR APPLICATION NUMBER:	08/860,082	
PRIOR FILING DATE:	1997-08-19	
PRIOR APPLICATION NUMBER:	PCT/US95/16542	
PRIOR FILING DATE:	1995-12-14	
PRIOR APPLICATION NUMBER:	IL 112022	
PRIOR FILING DATE:	1994-12-15	
PRIOR APPLICATION NUMBER:	IL 112692	
PRIOR FILING DATE:	1995-02-19	
NUMBER OF SEQ ID NOS:	2	
SOFTWARE:	Patentin version 3.0	
SEQ ID NO 2		
LENGTH:	256	
TYPE:	PRT	
ORGANISM:	Homo sapiens	
US-09-933-814-2		
Query Match	100.0%	Score 1302; DB 10; Length 256;
Best Local Similarity	100.0%	Pred. No. 2.8e-113;
Matches	256; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 VNQAPRCFRGGILGPIGRKRLASAPRTGARRAGQPPPLADPAMPDPLVLLHSYS 60	Sequence 30, Appl
DB	1 VNQAPRCFRGGILGPIGRKRLASAPRTGARRAGQPPPLADPAMPDPLVLLHSYS 60	Sequence 16, Appl
QY	61 SSLSSSEITELKFLCIGRVYKRLERVOGSDLFEMLLQNDLDFGHTELLRELLASLR 120	Sequence 2, Appl
DB	61 SSLSSSEITELKFLCIGRVYKRLERVOGSDLFEMLLQNDLDFGHTELLRELLASLR 120	Sequence 15, Appl
QY	121 HDLARRVDPEFGAAGAGAPGDEDCAPFNVICDVGWDRRLANQIAVSDPKIDSIDR 180	Sequence 27, Appl
DB	121 HDLARRVDPEFGAAGAGAPGDEDCAPFNVICDVGWDRRLANQIAVSDPKIDSIDR 180	Sequence 36, Appl

Db 121 HDLLRRVDEEAGAAAGAEEDLCAAFVYICDVGKDWRRRLAROLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLTIWKTEKENATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
Db 181 YPRNLTERVRESLTIWKTEKENATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
QY 241 MSPMSNSDASTSEAS 256
Db 241 MSPMSNSDASTSEAS 256

RESULT 2

US-09-824-134-2

Sequence 2, Application US/09824134

Patent No. US20020082401A1

GENERAL INFORMATION:

APPLICANT: WALLACH, David

BOLDIN, Mark

VARFOLOMEY, Eugene

METT, Igor

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1

RECEPTORS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824.134

FILING DATE: 03-Apr-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/860,082

FILING DATE: <Unknown>

APPLICATION NUMBER: IL 112022

FILING DATE: 15-DEC-1994

APPLICATION NUMBER: IL 112692

FILING DATE: 19-FEB-1995

APPLICATION NUMBER: IL 114615

FILING DATE: 16-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25, 618

REFERENCE/DOCKET NUMBER: WALLACH-16

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 256 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-824-134-2

Query Match

Best Local Similarity 100.0%; Score 1302; DB 10; Length 256;

Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECFFGGIILGPIGKRRDLAASEPRTEGARAGPOPPPLADPMDPFLVLLHSYS 60

Db 1 VNOAPECFFGGIILGPIGKRRDLAASEPRTEGARAGPOPPPLADPMDPFLVLLHSYS 60

QY 61 SSLSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHTELLRELLASLRR 120

Db 61 SSLSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDEEAGAAAGAEEDLCAAFVYICDVGKDWRRRLAROLKVSPTKIDSIEDR 180
Db 121 HDLLRRVDEEAGAAAGAEEDLCAAFVYICDVGKDWRRRLAROLKVSPTKIDSIEDR 180
QY 181 YPRNLTERVRESLTIWKTEKENATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
Db 181 YPRNLTERVRESLTIWKTEKENATVAHLVGLASCOMNIVADIVOEVOQARDLQNSGA 240
QY 241 MSPMSNSDASTSEAS 256
Db 241 MSPMSNSDASTSEAS 256

RESULT 3

US-09-952-768-64

Sequence 64, Application US/09952768

Patent No. US20020035242A1

GENERAL INFORMATION:

APPLICANT: Alnemrl, Ennad S.

Fernandes-Alnemrl, Teresa

Litwack, Gerald

Armstrong, Robert

Tomasselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,

NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: Suite 6300, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..84

OTHER INFORMATION: /note="human PADD"

SEQUENCE DESCRIPTION: SEQ ID NO: 64:

US-09-952-768-64

Query Match

Best Local Similarity 31.1%; Score 405; DB 10; Length 84;

Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108

Db 1 MDPLVLLHSVSSSSSELTCLKLGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 60

```
OY . 109 ELRELLASLRHDLRRVDFEA 132  
      |||||  
Db . 61 ELRELLASLRHDLRRVDFFEA 84
```

RESULT 4
US-09-410-194-9
; Sequence 9, Application US/09410194
; Patent No. US20020095030A1

GENERAL INFORMATION:
 APPLICANT: Tschopp, Jurg
 APPLICANT: Thome, Margot
 APPLICANT: Burns, Kimberly
 APPLICANT: Imbler, Martin
 APPLICANT: Hahnel, Michael
 APPLICANT: Schroter, Michael
 APPLICANT: Schneider, Pascal
 APPLICANT: Bodmer, Jean- Luc
 APPLICANT: Steinert, Veronique
 APPLICANT: Rimoldi, Donata
 APPLICANT: Hofmann, Kay
 APPLICANT: French, E. Iars
 TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
 FILE REFERENCE: 11141-002001

```

? CURRENT APPLICATION NUMBER: US-09/410-194-9
? CURRENT FILING DATE: 1999-09-30
? PRIOR APPLICATION NUMBER: PCT/EP98/01857
? PRIOR FILING DATE: 1998-03-31
? PRIOR APPLICATION NUMBER: GERANY 197 13
? PRIOR FILING DATE: 1997-04-01
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 9
? LENGTH: 81
? TYPE: prt
? ORGANISM: Homo sapiens
US-09-410-194-9

```

Query Match	30.0%;	Score 390;	DB 10;	Length 81;
Best Local Similarity	98.8%;	Pred. No. 4,2e-29;		
Matches	80;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0
QY	49	MDPFLVLLHSVSSSSLSSELTETLKCICGVRVKKRLERVOGSLDLFSMLEQNDLEPGHT	108	
DB	1	MDPFLVLLHSVSSSSLSSELTETLKCICGVRVKKRLERVOGSLDLFSMLEQNDLEPGHT	60	
QY	109	ELLRELLASIRRHDLIRVDD	129	
DB	61	ELLRELLASIRRHDLIRVDD	81	

RESULT 5
US-10-001-254-39
; Sequence 39, Application US/10001254
; Publication No. US20030069702A1

GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sung Hyung
APPLICANT: both, Wilfried
APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702.1e1 Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001.254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 39
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-39

```

Query Match	29.68;	Score 386;	DB 9;	Length 82;
Best Local Similarity	96.4%;	Pred. No. 1e-28;		
Matches	80;	Conservative	1;	Mismatches 0; Indels 2; Gaps 1

QY	49	MDFVLTLHVSSSLSSELTEKFLC
Db	1	MDFVLTLHVSSSLSSELTEKFLC
QY	109	EILRELTASLRDDLRYVDFFE 131
Db	59	EILRELTASLRDDLRYVDFFE 81

RESULT 6
US-10-112-793-25
; Sequence 25, Application US/10112793
; Publication NO. US20020192729A1
; GENERAL INFORMATION:

APPLICANT: ASHKENAZI, AVI J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/928,693A

APPLICATION NUMBER: US970602670
 FILING DATE: 31-Mar-1997
 APPLICATION NUMBER: 08/625328
 FILING DATE: 1-Apr-1996
 APPLICATION NUMBER: 08/710802
 FILING DATE: 23-Sep-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marchand, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1007P1
 TELECOMMUNICATION INFORMATION:
 ET-1022

TELEPHONE: 650/22-3310
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 US-10-112-793-25

Query Match 29.3%; Score 382; DB 9; length 74;
Best Local Similarity 100.0%; Pred. No. 2,1e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 212 ALRSCOMNLVADLV 225
Db 61 ALRSCOMNLVADLV 74

RESULT 7

US-10-287-594-5
Sequence 5, Application US/10287594
Publication No. US20030096288A1
GENERAL INFORMATION:
APPLICANT: Nt, Jjian
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: RAIDD, A NO. US20030096288A1el Death Adaptor Molecule
FILE REFERENCE: 1488, 0860002
CURRENT FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US/09/545,605
PRIOR FILING DATE: 2001-04-07
PRIOR APPLICATION NUMBER: 08/995,159
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-594-5

Query Match 29.3%; Score 382; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 2, 1e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 152 ICDNVGKDMRLAQLKVSIDRYPRNLTERRVRESLRIMKTEKENATVAHLVG 211
Db 1 ICDNVGDMRLAQLKVSIDRYPRNLTERRVRESLRIMKTEKENATVAHLVG 60

Oy 212 ALRSCOMNLVADLV 225
Db 61 ALRSCOMNLVADLV 74

RESULT 8

US-10-001-254-35
Sequence 35, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Florentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfried
APPLICANT: Stenner-Ilewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-254-35

Query Match 28.3%; Score 369; DB 9; Length 77;
Best Local Similarity 98.7%; Pred. No. 3, 6e-27;

Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 49 MDPELVILHSVSSLSSELTLEKFLCIGRVYKRLERVOSGIDLFSMLEQNDLEPGHT 108
Db 1 MDPELVILHSVSSLSSELTLEKFLCIGRVYKRLERVOSGIDLFSMLEQNDLEPGHT 60

Oy 109 ELRELLASLRHHDLR 125
Db 61 ELRELLASLRHHDLR 77

RESULT 9

US-10-035-408-5
Sequence 5, Application US/10035408
Patent No. US20020123117A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark P.
VARPOLOMEY, Eugene E.
PANCER, Zeev
METZ, Igor
GONCHAROV, Tanya M.
WEINMURZEL, Henry
TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/035,408
FILING DATE: 04-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 737-3528
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-035-408-5

Query Match 24.4%; Score 318; DB 12; Length 62;
Best Local Similarity 100.0%; Pred. No. 1, 5e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 160 WRRLAROLKVSIDRYPRNLTERRVRESLRIMKTEKENATVAHLVGALRSCOMN 219
Db 1 WRRLAROLKVSIDRYPRNLTERRVRESLRIMKTEKENATVAHLVGALRSCOMN 60

OY 220 LV 221
DB 61 LV 62

RESULT 10

US-10-068-564-48
Sequence 48, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
APPLICANT: Fernandez-Alnemrl, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068, 564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-10-068-564-48

Query Match 9.9%; Score 128.5; DB 9; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPELVLLHSVSSLSSELTLEKFCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDAIAEELGSEDLAALFKFLDLYTPHKKLTIEDAKFLRLRKGMLEEGNTL 59

OY 109 ELRELLASLRHDL 124
DB 60 SFLKELLFHISRMDL 75

RESULT 11

US-09-989-903-48
Sequence 48, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
APPLICANT: Fernandez-Alnemrl, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989, 903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 250
TYPE: PRT
ORGANISM: Mus musculus
US-09-989-903-48

Query Match 9.9%; Score 128.5; DB 10; Length 250;
Best Local Similarity 40.8%; Pred. No. 0.0004; Indels 1; Gaps 1;
Matches 31; Conservative 12; Mismatches 32;

OY 49 MDPELVLLHSVSSLSSELTLEKFCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHT 108
DB 1 MD-PQSLDAIAEELGSEDLAALFKFLDLYTPHKKLTIEDAKFLRLRKGMLEEGNTL 59

OY 109 ELRELLASLRHDL 124
DB 60 SFLKELLFHISRMDL 75

RESULT 12

US-09-410-194-7
Sequence 7, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Tschopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Imley, Martin
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lairs
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410, 194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-7

Query Match 9.4%; Score 122; DB 10; Length 177;
Best Local Similarity 28.8%; Pred. No. 0.001; Indels 16; Gaps 4;
Matches 38; Conservative 23; Mismatches 55;

OY 56 LHSVSSLSSELTLEKFCIGRVYKRLERVOGSLDLSMLLEQNDLEPGHTLEHRL 115
DB 7 LYDIGEQLDSIEDLSIFSLDLYTPKQKQEPKXALMFORLQKRMLEESNTSLKRL 66

OY 116 ASLRHDL-----RRDDFAGAAAGAPGEEDICAAFNVCNDVQKMR-----L 163
DB 67 FRINRLDLYLTATRKEMEREL--QTPGRACI-SAYRYMXYOISSEVSRSLSRPF 122

OY 164 ARLKVSPTKID 175
DB 123 LLOEISCKRID 134

RESULT 13

US-09-009-893-3
Sequence 3, Application US/09009893
Publication No. US20030087339A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: DIXIT, VISHVA M.
APPLICANT: GENTZ, REINER L.
APPLICANT: KENNY, JOSEPH J.
TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,893
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFER, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-3

Query Match
Best Local Similarity 28.8%; Score 122; DB 9; Length 478;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

QY 56 LHSVSSSSSETEKFLCIGRVVKKLERVSGIDLSMLLEQNDLPGHTELLRELL 115
DB 7 LVDIGQDSEDLASKFLSLDVIYIPQRKQEPIDALMFORLQEKMLESNLSFLKELL 66
QY 116 ASLRHDDL-----RRVDFEAGAAGAAGEEDLCARFVYCDNVGKDMRR-----L 163
DB 67 FRNRDLILITYINTRKEEMEREL---QTPGRAQI-SAYRVMLYQISEEVSSELSRFRF 122
QY 164 ARQLKVSDFKID 175
DB 123 LQAEISKCKLD 134

RESULT 14
US-09-410-194-20
Sequence 20, Application US/09410194
Patent No. US20020095030A1
GENERAL INFORMATION:
APPLICANT: Techopp, Jurg
APPLICANT: Thome, Margot
APPLICANT: Burns, Kimberly
APPLICANT: Immler, Marten
APPLICANT: Hahne, Michael
APPLICANT: Schroter, Michael
APPLICANT: Schneider, Pascal
APPLICANT: Bodmer, Jean-Luc
APPLICANT: Steiner, Veronique
APPLICANT: Rimoldi, Donata
APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 479

TYPE: PRT
ORGANISM: Homo sapiens
US-09-410-194-20

Query Match
Best Local Similarity 28.8%; Score 122; DB 10; Length 479;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

QY 56 LHSVSSSSSETEKFLCIGRVVKKLERVSGIDLSMLLEQNDLPGHTELLRELL 115
DB 7 LVDIGQDSEDLASKFLSLDVIYIPQRKQEPIDALMFORLQEKMLESNLSFLKELL 66
QY 116 ASLRHDDL-----RRVDFEAGAAGAAGEEDLCARFVYCDNVGKDMRR-----L 163
DB 67 FRNRDLILITYINTRKEEMEREL---QTPGRAQI-SAYRVMLYQISEEVSSELSRFRF 122
QY 164 ARQLKVSDFKID 175
DB 123 LQAEISKCKLD 134

RESULT 15
US-09-952-768-66
Sequence 66, Application US/09952768
Patent No. US20020035242A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140,424C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
FEATURE:
NAME/KEY: peptide
LOCATION: 1-75
OTHER INFORMATION: /note="Mch5 A"
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-952-768-66

Query Match
Best Local Similarity 39.1%; Score 117; DB 10; Length 75;
Matches 27; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

OY 56 LHSVSSLSSELTELKFCIGRVKRLERVOGGLDLSMTLEONDLPEGHTELLREL 115
 Db 4 LYDIGEQLDSEDLASLFLSLDPTIPQRKQEPKDALMLFQRLQPKRRLLESNLSFLKELL 63

OY 116 ASLRHDLL 124

Db 64 FRINRDL 72

Search completed: June 19, 2003, 10:44:49
 Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:35:05 ; Search time 18 Seconds
(without alignments)
1367.245 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VQNAPECRGCGGILGPKR.....RSGAMSPMSWSDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	79.9	208	2 A56912	FADD protein - human
2	121.5	9.3	1856	2 B35049	ankyrin 1, erythro
3	121.5	9.3	1880	2 A35049	ankyrin 1, erythro
4	121.5	9.3	1881	1 SJHUK	ankyrin 1, erythro
5	117.5	9.0	1848	2 S37771	ankyrin, erythrocy
6	117.5	9.0	1862	2 I49502	ankyrin - mouse
7	115.5	8.9	655	2 I49289	receptor interacti
8	111.5	8.6	671	2 T09479	serine/threonine p
9	103	7.9	2039	2 T15347	ankyrin-related un
10	99	7.6	919	2 F83257	hypothetical prote
11	99	7.6	1955	2 T30934	myosin-like protei
12	99	7.6	3924	2 S37431	ankyrin 2, neuona
13	98.5	7.6	4644	1 A38905	dynelin heavy chain
14	97	7.5	622	2 A84280	glu-tRNA amidotran
15	96.5	7.4	1162	2 T49191	hypothetical prote
16	96	7.3	647	2 C83012	probable chemotaxi
17	95.5	7.3	497	2 F83087	RNA polymerase sig
18	95.5	7.3	509	2 H87685	conserved hypotet
19	95	7.3	406	2 G70639	hypothetical prote
20	95	7.3	414	2 T35625	probable sensor-11
21	94.5	7.2	497	2 A53373	IFON protein - pse
22	94	7.2	1534	2 A56734	ribosome receptor,
23	93.5	7.2	324	2 JC2395	Fas antigen precut
24	91.5	7.0	470	2 F70621	probable argin prot
25	91.5	7.0	763	2 A82863	hypothetical prote
26	91	7.0	809	2 G75605	hypothetical prote
27	91	7.0	1029	2 H96658	hypothetical prote
28	90.5	7.0	130	2 S55385	PA-15 protein - m
29	90.5	7.0	411	2 S45318	keratin 12 - rabbi

30	90.5	7.0	2427	2 T16613	hypothetical prote
31	90	6.9	520	2 S35575	myosin heavy chain
32	90	6.9	725	2 A47168	cardiac morphogene
33	89.5	6.9	536	1 A47190	transducer protein
34	89.5	6.9	536	2 E84318	Hrl1 transducer (1
35	89.5	6.9	1816	1 S68960	laminin alpha-4 ch
36	89	6.8	483	2 A55033	keratin 12 - mouse
37	88.5	6.8	130	2 S5384	PA-15 protein - h
38	88.5	6.8	807	2 T00980	hypothetical prote
39	88.5	6.8	892	1 FADDA	alpha actinin 1 -
40	88.5	6.8	1927	2 A59236	embryonic muscle m
41	87.5	6.7	294	2 A11617	protein secretion
42	87.5	6.7	433	2 A32992	cyclin B1 - human
43	87.5	6.7	1732	2 G84664	hypothetical prote
44	87.5	6.7	3433	2 S28381	utrophin - human
45	87.5	6.7	4377	2 A55575	ankyrin 3, long sp

ALIGNMENTS

RESULT 1

A56912

FADD protein - human

N:Alternate names: FAS-associating death domain containing protein FADD; mediator of

C:Species: Homo sapiens (man)

C>Date: 11-Aug-1995 #sequence, revision 11-Aug-1995 #text, change 01-Dec-2000

C/Accession: A56912; I38041

R:Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.

Cell 81, 505-512, 1995

A>Title: FADD, a novel death domain-containing protein, interacts with the death doma

A:Reference number: A56912; MUID:95277837; PMID:7538907

A:Accession: A56912

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <CHI>

A:Cross-references: GB:U24231; NID:9809486; PID:AAA86517.1; PID:9809487

R:Boldin, M.P.; Varfolomeev, E.E.; Pancar, Z.; Mett, I.L.; Camonis, J.H.; Wallach, D.

J. Biol. Chem. 270, 7795-7798, 1995

A>Title: A novel protein that interacts with the death domain of Fas/AP01 contains a

A:Reference number: I38041; MUID:95229578; PMID:7536190

A:Accession: I38041

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-31, V, 33-208 <RES>

C:Cross-references: EMBL:X84709; NID:9791037; PID:CAA59197.1; PID:9791038

C:Genetics:

A:Gene: GDB:FADD; MORT1

A:Cross-references: GDB:1320394

C:Superfamily: receptor-induced toxicity mediator MORT1

C:Keywords: apoptosis

Query Match 79.9%; Score 1040; DB 2; Length 208;

Best Local Similarity 99.5%; Pred. No. 2.3e-75;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	49	MDPFLVILHSVSSLSSELTETKFLCLGRVYKRLERVOGDLFLSLLEQNDLEPHT	108
DB	1	MDPFLVILHSVSSLSSELTETKFLCLGRVYKRLERVOGDLFLSLLEQNDLEPHT	60
QY	109	ELRELASLRRLHDLRRVDFEAGAAAGAPGEDICAAFNVICDNVGRRLAROLK	168
DB	61	ELRELASLRRLHDLRRVDFEAGAAAGAPGEDICAAFNVICDNVGRRLAROLK	120
QY	169	VSDTKIDSIEDRYRNLTERVRESLRITWKTEKENATVAHLVGLRSCQNLVADLVQEV	228
DB	121	VSDTKIDSIEDRYRNLTERVRESLRITWKTEKENATVAHLVGLRSCQNLVADLVQEV	180
QY	229	QOARDLONRSGAMSPMSWSDASTSEAS	256
DB	181	QOARDLONRSGAMSPMSWSDASTSEAS	208

RESULT 2
B35049
ankyrin 1, erythrocyte splice form 3 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C:Accession: B35049
R:Lambert, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: B35049
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1856 <AM>
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <AM>
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
Query Match 9.3%; Score 121.5; DB:2; Length 1856;
Best Local Similarity 27.2%; Pred. No. 0.3;
Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
OY 137 GAAGGEEICAAFNVCIDNVGKDKRRLAROLKVSDFDKTSIEDYPRRLTRVRESLRIM 196
DB 1395 GSLSGTQAEKMAVISHLGLSWAELEKLEQSVEDINRIRVENPNSLSESVALLNIM 1454
OY 197 KTEKENATVAHLVGLRSCOMNLVADLYQ-EVQOARDLQ-----NNSGAMSPMSNSD 249
DB 1455 VIRGQNNMNTLTALQSIDRGEIVNKLBSGSGSRNLKRDHRHTDYSLSQSNMGY 1514
OY 250 ASTSE 254
DB 1515 SSLAD 1519
RESULT 3
A35049
ankyrin 1, erythrocyte splice form 2 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
C:Accession: A35049

R:Lambert, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: A35049
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1880 <AM>
A:Cross-references: GB:M28880
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; cytoskeleton
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <AM>
F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
Query Match 9.3%; Score 121.5; DB:2; Length 1880;
Best Local Similarity 27.2%; Pred. No. 0.3;
Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
OY 137 GAAGGEEICAAFNVCIDNVGKDKRRLAROLKVSDFDKTSIEDYPRRLTRVRESLRIM 196
DB 1395 GSLSGTQAEKMAVISHLGLSWAELEKLEQSVEDINRIRVENPNSLSESVALLNIM 1454
OY 197 KTEKENATVAHLVGLRSCOMNLVADLYQ-EVQOARDLQ-----NNSGAMSPMSNSD 249
DB 1455 VIRGQNNMNTLTALQSIDRGEIVNKLBSGSGSRNLKRDHRHTDYSLSQSNMGY 1514
OY 250 ASTSE 254
DB 1515 SSLAD 1519
RESULT 4
SUBUR
ankyrin 1, erythrocyte splice form 1 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S08275; A33219; PC2220; A35443
R:Jux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A:Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
A:Reference number: S08275; MUID:90158830; PMID:2137537
A:Accession: S08275
A:Molecule type: mRNA
A:Residues: 1-1881 <L01>

A:Cross-references: EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
 A:Accession: A33219
 A:Molecule type: Protein
 A:Residues: 277, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X',
 X, 1367, 1383-1427, 1601-1630, 1686-1698, 'D', 1700; 1763-1772 <LUX>
 A:Note: 845-Ary and 1392-Thr were also found
 R:Herzmann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994
 A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
 A:Reference number: PC2220; MUID:95077348; PMID:7526850
 A:Accession: PC2220
 A:Molecule type: protein
 A:Residues: 910-929 <HER>
 R:David, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
 A:Reference number: A35443; MUID:90285190; PMID:2141335
 A:Accession: A35443
 A:Molecule type: protein
 A:Residues: 'X', 5, 'X', 7-12, 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814, 862-863,
 C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 9p11.2-9p11.2
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing; phosphoprotein
 F:2-1881/Product: ankyrin 1, erythrocyte form 1 status predicted <ANT1>
 F:2-1511,1675-1881/Product: ankyrin 2, erythrocyte status predicted <ANT2>
 F:2-827/Region: anion exchange protein binding
 F:44-76/Domain: ankyrin repeat homology <AN01>
 F:77-109/Domain: ankyrin repeat homology <AN02>
 F:110-142/Domain: ankyrin repeat homology <AN03>
 F:143-111/Domain: ankyrin repeat homology <AN04>
 F:172-204/Domain: ankyrin repeat homology <AN05>
 F:205-237/Domain: ankyrin repeat homology <AN06>
 F:238-270/Domain: ankyrin repeat homology <AN07>
 F:271-303/Domain: ankyrin repeat homology <AN08>
 F:304-336/Domain: ankyrin repeat homology <AN09>
 F:337-369/Domain: ankyrin repeat homology <AN10>
 F:370-402/Domain: ankyrin repeat homology <AN11>
 F:403-435/Domain: ankyrin repeat homology <AN12>
 F:436-468/Domain: ankyrin repeat homology <AN13>
 F:469-501/Domain: ankyrin repeat homology <AN14>
 F:502-534/Domain: ankyrin repeat homology <AN15>
 F:535-567/Domain: ankyrin repeat homology <AN16>
 F:568-600/Domain: ankyrin repeat homology <AN17>
 F:601-633/Domain: ankyrin repeat homology <AN18>
 F:634-666/Domain: ankyrin repeat homology <AN19>
 F:667-699/Domain: ankyrin repeat homology <AN20>
 F:700-732/Domain: ankyrin repeat homology <AN21>
 F:733-765/Domain: ankyrin repeat homology <AN22>
 F:766-798/Domain: ankyrin repeat homology <AN23>
 F:828-1382/Domain: 62K status predicted <DOM2>
 F:828-1382/Region: spectrin binding
 F:1383-1881/Domain: 55K status predicted <DOM3>
 Query Match 9.3%; Score 121.5; DB 1; Length 1881;
 Best Local Similarity 27.2%; Pred. No. 0.3;
 Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;
 Oy 137 GAAGGEBDCAAFVYICNVCKDKRRLAROLKVSDFKIDSIEDRYPRNLTERRVRESLRIMKTERENAVAHV 196
 Db 1395 GSLSGTEQAEKMAVISHLQISVAELARELFQSFEDINRRVNPNSLIDQSVALLIMV 1454
 Oy 197 KTEKENATVAHLVGLARSCOMNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSNSD 249
 Db 1455 VIRGQANMMENTLTAQSIDRGELVNMLEBSGSRNLKDFDRRTDIDYLSPSQANNGY 1514
 Oy 250 ASTSE 254
 Db 1515 SSIOD 1519

RESULT 5
 S37771
 ankyrin, erythrocyte - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
 A:Accession: S37771
 R:Bitkemeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
 J. Biol. Chem. 268, 9533-9540, 1993
 A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found
 A:Reference number: S37771; MUID:93252825; PMID:8486643
 A:Accession: S37771
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1848 <BIR>
 A:Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:48-80/Domain: ankyrin repeat homology <AN01>
 F:81-113/Domain: ankyrin repeat homology <AN02>
 F:114-146/Domain: ankyrin repeat homology <AN03>
 F:147-175/Domain: ankyrin repeat homology <AN04>
 F:176-208/Domain: ankyrin repeat homology <AN05>
 F:209-241/Domain: ankyrin repeat homology <AN06>
 F:242-274/Domain: ankyrin repeat homology <AN07>
 F:275-307/Domain: ankyrin repeat homology <AN08>
 F:308-340/Domain: ankyrin repeat homology <AN09>
 F:341-373/Domain: ankyrin repeat homology <AN10>
 F:374-406/Domain: ankyrin repeat homology <AN11>
 F:407-439/Domain: ankyrin repeat homology <AN12>
 F:440-472/Domain: ankyrin repeat homology <AN13>
 F:473-505/Domain: ankyrin repeat homology <AN14>
 F:506-538/Domain: ankyrin repeat homology <AN15>
 F:539-571/Domain: ankyrin repeat homology <AN16>
 F:572-604/Domain: ankyrin repeat homology <AN17>
 F:605-637/Domain: ankyrin repeat homology <AN18>
 F:638-670/Domain: ankyrin repeat homology <AN19>
 F:671-703/Domain: ankyrin repeat homology <AN20>
 F:704-736/Domain: ankyrin repeat homology <AN21>
 F:737-769/Domain: ankyrin repeat homology <AN22>
 F:770-802/Domain: ankyrin repeat homology <AN23>
 Query Match 9.0%; Score 117.5; DB 2; Length 1848;
 Best Local Similarity 27.9%; Pred. No. 0.62;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;
 Oy 151 VICDVGDMWRRLAOLKVSDFKIDSIEDRYPRNLTERRVRESLRIMKTERENAVAHV 210
 Db 1421 VIREHGLSVAELARELFQSFEDINRRVNPNSLIDQSVALLIMV 1480
 Oy 211 GALSRCOMNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSNSDASTSE 254
 Db 1481 TALRIDRSEIYNMLEVSGSRNLKPRRRHDFRYSLSPSQVNYSSIOD 1531
 RESULT 6
 149502
 ankyrin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 A:Accession: 149502
 R:White, R.A.; Bitkemeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
 Mamm. Genome 3, 281-285, 1992
 A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
 A:Reference number: 149502; MUID:92245717; PMID:1386265
 A:Accession: 149502
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1862 <RBS>
 A:Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940
 C:Genetics:
 A:Gene: Ank-1
 C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing
 F:40-72/Domain: ankylrin repeat homology <AN01>
 F:73-105/Domain: ankylrin repeat homology <AN02>
 F:106-138/Domain: ankylrin repeat homology <AN03>
 F:139-167/Domain: ankylrin repeat homology <AN04>
 F:168-200/Domain: ankylrin repeat homology <AN05>
 F:201-233/Domain: ankylrin repeat homology <AN06>
 F:234-266/Domain: ankylrin repeat homology <AN07>
 F:267-299/Domain: ankylrin repeat homology <AN08>
 F:300-332/Domain: ankylrin repeat homology <AN09>
 F:333-365/Domain: ankylrin repeat homology <AN10>
 F:366-398/Domain: ankylrin repeat homology <AN11>
 F:399-431/Domain: ankylrin repeat homology <AN12>
 F:432-464/Domain: ankylrin repeat homology <AN13>
 F:465-497/Domain: ankylrin repeat homology <AN14>
 F:498-530/Domain: ankylrin repeat homology <AN15>
 F:531-563/Domain: ankylrin repeat homology <AN16>
 F:564-596/Domain: ankylrin repeat homology <AN17>
 F:597-629/Domain: ankylrin repeat homology <AN18>
 F:630-662/Domain: ankylrin repeat homology <AN19>
 F:663-695/Domain: ankylrin repeat homology <AN20>
 F:696-728/Domain: ankylrin repeat homology <AN21>
 F:729-761/Domain: ankylrin repeat homology <AN22>
 F:762-794/Domain: ankylrin repeat homology <AN23>

Query Match 9.0%; Score 117.5; DB 2; Length 1862;
 Best Local Similarity 27.9%; Pred. No. 0.62;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;

OY 151 VICNVGDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKNTEKENVATVHL 210
 DB 1405 VIRHHLDSNAELARELQFSTEDINRIVENPSLLQSTLLTLWLWDRENNKMENTLY 1464
 OY 211 GALSRCOMNLVADLVQ-EVQOARDLQ-----NRSGAMPSPMSWSDASTSE 254
 DB 1465 TALRNIDRSEIVNLTGSGRSRLKPKERRRGDRREYLSLSPQVNGYSLQD 1515

RESULT 7
 149299
 Receptor interacting protein RIP - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
 C:Accession: I49299
 R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
 Cell 81, 513-523, 1995
 A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
 A:Reference number: A56913; MUID:95277838; PMID:7538908
 A:Accession: I49299
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-656 <RES>
 A:Cross-references: EMBL:U25995; NID:9829618; PIDN:AA60487.1; PID:9829619
 C:Genetics:
 A:Gene: RIP
 A:Superfamily: protein kinase homology
 F:15-293/Domain: protein kinase homology <KIN>

Query Match 8.9%; Score 115.5; DB 2; Length 656;
 Best Local Similarity 34.9%; Pred. No. 0.24; Indels 3; Gaps 3;
 Matches 29; Conservative 22; Mismatches 29;

OY 150 NVICDNYGDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKNTEKENVATVHL 207
 DB 573 NPIRENIGRQWKNCAKRLGFTESQIDEIDHYERDGLKEKYOMLQKWLMEGKATVYG 632
 OY 208 HLVGAL-RSCOMNLVADLVQEVQ 229
 DB 633 KLAQALHQCRRIDLNLHLIRASQ 655

RESULT 8
 109479

serine/threonine protein kinase (EC 2.7.1.1-) RIP - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
 C:Accession: T09479; I38992
 R:Huang, J.; Hsu, H.; Balchwal, V.R.; Goeddel, D.V.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: Z1685
 A:Accession: T09479
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-671 <HVA>
 A:Cross-references: EMBL:U50062; NID:93426026; PID:93426027
 R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
 Cell 81, 513-523, 1995
 A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
 A:Reference number: A56913; MUID:95277838; PMID:7538908
 A:Accession: I38992
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 300-513; 'S', 515-671 <RES>
 A:Cross-references: EMBL:U25994; NID:9829616; PIDN:AA650137.1; PID:9829617
 C:Genetics:
 A:Gene: RIP
 C:Keywords: ATP binding; phosphotransferase

Query Match 8.6%; Score 111.5; DB 2; Length 671;
 Best Local Similarity 36.4%; Pred. No. 0.51;
 Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;

OY 152 ICDNVGDMRLARLQKVSPTKIDSIEDRYPRNLTEVRSLTKMKNTEKENVATVHL 209
 DB 590 IRENIGRQWKNCAKRLGFTESQIDEIDHYERDGLKEKYOMLQKWLMEGKATVYGL 649
 OY 210 VGALRSC-OMNLVADLV 225
 DB 650 AQAALHQCRRIDLNLHLIRASQ 666

RESULT 9
 115347
 ankylrin-related unc-44 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Aug-2002
 C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
 R:Gallung, S.
 submitted to the EMBL Data Library, February 1996
 A:Description: The sequence of C. elegans coemid B0350.
 A:Reference number: Z18332
 A:Accession: T15347
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2039 <GAT>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208873; PIDN:AAA93443.1
 A:Accession: T15346
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1000; 'SKLQHRT', 1002-1718; 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, '32', 'S', 2034-2035; 'GSPTRRVEPEHRSQHEHDEGST' <GA2>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208875; PIDN:AAA93445.1
 A:Accession: T15344
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718; 'KW', 1903-1905; 'NRLADESSPS', 1916-1917; 'QRSTVAESTSEQVE', 1934-1935; <GA3>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208874; PIDN:AAA93444.1
 A:Accession: T15345
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718; 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAORS', 1950, '1956-1957, 'EK
 PTRRVEPEHRSQHEHDEGST' <GA4>
 A:Cross-references: EMBL:U50071; NID:91208871; PID:91208876; PIDN:AAA93446.1
 R:Otsuka, A.J.; Franco, R.; Yang, B.; Shlm, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontreku
 J. Cell Biol. 129, 1081-1092, 1995.

```

QY      24 RASSPREDGARRAGROPEL---ADPADPPLVLYHSVSSLSSEELTE-----LK 72
DB      145 APVSPAPRTGAPRAQOAPAPVPTTTPAGSDTTKTVSNDLTWELTAQNRNRDVSVPQAMLA 204
QY      73 F--ICLGRVVKKLEEVOSGLDLFSMLLEQNDLEPEGTELLRELLASLRHDLIRYDVF 130
DB      205 FOELNPGAFVQDNINRKLKSG--QVLRPTPEQOMLESPRALSGVQAQONOSWGRSRNPAG 263

```

[illegible]

Db 36332 AEIDQTTLDHSEG 3645

RESULT 13

A38905

N:Contains: dynein heavy chain, cytosolic - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Apr-1994 #sequence.revision 02-May-1994 #text.change 19-Apr-2002

C:Accession: A38905; 158139

R:Zhang, Z.; Tanaka, Y.; Nonaka, S.; Aizawa, H.; Kawasaki, H.; Nakata, T.; Hirokawa, Proc. Natl. Acad. Sci. U.S.A. 90, 7928-7932, 1993

A:Title: The primary structure of rat brain (cytoplasmic) dynein heavy chain, a cytop

A:Reference number: A38905; MUID:93376715; PMID:7690137

A:Accession: A38905

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-4644 <ZNA>

A:Cross-references: GB:013896; NID:g402527; PIDN:BA02996.1; PID:g402528

R:Matsumi, A.; Paschal, B.M.; Mazumdar, M.; Vallée, R.B.

N:Neuron 10, 787-796, 1993

A:Title: Molecular cloning of the retrograde transport motor cytoplasmic dynein MAP 1

A:Reference number: 158139; MUID:93264075; PMID:7684232

A:Accession: 158139

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1033, 'MF', 1026-1771, 'D', 1773-2097, 'A', 2099-2138, 'V', 2140-2174, 'A', 2176

44 <RES>

A:Cross-references: GB:I080505; NID:g294542; PIDN:AAA41103.1; PID:g294543

C:Superfamily: dynein heavy chain, cytosolic

C:Keywords: ATP; blocked amino end; heterotrimer; hydrolyase; microtubule binding; r

F:1904-1911,Region: nucleotide-binding motif A (P-loop)

F:2222-2229,Region: nucleotide-binding motif A (P-loop)

F:2953-2600,Region: nucleotide-binding motif A (P-loop)

F:2935-2942,Region: nucleotide-binding motif A (P-loop)

F:1910,Binding site: ATP (Lys) #status predicted

F:2228,Binding site: ATP (Lys) #status predicted

F:2599,Binding site: ATP (Lys) #status predicted

F:2941,Binding site: ATP (Lys) #status predicted

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Query March 7.6%: Score 98.5; DB 1; Length 4644;
Best Local Similarity 23.5%: Pred. No. 64;
Match 59; Conservative 32; Mismatches 83; Indels 77; Gaps 12;

QY 53 LVLTSHVSSSLSEELTELKFLCGRVYKRLERVOSSL-----DL 93
| : : : | | | : | : : | : |
DB 376 LVLYEALSRDLSOQLKLTGRKLMHVAEEFEKVMACFEVPTWDEYEKLYLRLDI 435
| : : : | | | : | : : | : |
QY 94 FSMLEON-----DLPEGTEL---LRELIASLRHHLLR---RVDDFEAGAAA---G 137
| : : : | : : : | : : : | : : : | : : : | : : : |
DB 436 VKRRREELTKVMWRINPAHRLQARLDQMRKFRROHEQLRAVIVRVLPQTAVAAQONOG 495
| : : : | : : : | : : : | : : : | : : : | : : : |
QY 138 AARPEEDLCAA-----FNVICNV---GKD-----WRRLAQLKYSYD 171
| : : : | : : : | : : : | : : : | : : : | : : : |
DB 496 EAPRPDDKVAEVLFDADAANAIEVNIATAYNVKVEVDGLDVSKEGTEAME---AAMKRYD 552
| : : : | : : : | : : : | : : : | : : : | : : : |
QY 172 TKDISIEDRYPRNLTERRESLRITMKNT-----EKENATVA---HLVGALRSOMNLVA 222
| : : : | : : : | : : : | : : : | : : : | : : : |
DB 553 ERIDRVERA---ITARLDQLGTAKNANEKFRITFSRNALFVRPHINGALREYOTOLIQ 608
| : : : | : : : | : : : | : : : | : : : | : : : |
QY 223 DLVQEVQOARD 233
| : : : | : : : | : : : | : : : | : : : | : : : |
DB 609 RVKDDIESLHD 619
| : : : | : : : | : : : | : : : | : : : | : : : |

```

RESULT 14
AB4290
Glu-TRNA amidotransferase [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: AB4290
R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Lelthausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; J

Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MID:20504483; PMID:11016950
A:Accession: A84290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-622 <STO>
A:Cross-References: GB:AE004437; NID:g10580865; PID:NAC19685.1; GSPDB:GN00138
C:Genetics:
A:Gene: gatB1

Query Match 7.5%; Score 97; DB 2; Length 622;

Best Local Similarity 24.3%; Pred. No. 6.5;

Matches 64; Conservative 31; Mismatches 96; Indels 72; Gaps 14;

QY 17 LGRRDLARASEP-RTEGARRAGPP--RPLAD-----PANDPLVLLHSVSSL 63
DB 391 VAEKRAETAMAGVPEEREGANDGETSKYLPFGAARMYPETDVPYDP-----DP 440
QY 64 SSELTELFCLGKRVKKRLERVOGGLDFSMLEQ-----NDLEPG-----H 107
DB 441 SAVERPEL-----LTEKVEREQADFLDAGIAQVAYGRWQLFEQOVEAGVDATLA 492
QY 108 TELRELLASLRHDL-LRVDDFEAGAAAG-----AAGEEDCAAFNYICDVGKD 159
DB 493 AQLTESTVTELRDDVPVGLTDHFRGYLGIVADGLAQEGVELLAA--LAEPGSD 549
QY 160 WRRLAROLKVSPTKIDSIDR---YPRNLTERVRESLRIMKTEKENATVAHLVGALRS 215
DB 550 PVLAEELGLGSAEDVEAVYGVYERNSDVAABGKAF-----SALMGCKGALRG 603
QY 216 COMNLVADLYOEVOGARDLQNRS 238
DB 604 ---KADGDLVSEYLR-EIQQRS 622

RESULT 15

T49191

hypothetical protein MAA21.130 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49191

R:Reger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: 225018

A:Accession: T49191

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1162 <RIE>

A:Cross-References: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.130

A:Experimental source: cultivar Columbia; BAC clone MAA21

C:Genetics:

A:Gene: ATSP:MAA21.130

A:Map position: 3

A:introns: 975/1

C:Superfamily: Arabidopsis thaliana hypothetical protein MAA21.130

Query Match 7.4%; Score 96.5; DB 2; Length 1162;

Best Local Similarity 22.6%; Pred. No. 16;

Matches 59; Conservative 35; Mismatches 98; Indels 69; Gaps 12;

QY 8 RFGG-----GILGPIGKRRDLARASEPRTGARRAGPPPLAD 46
DB 108 RFGGPNDRGVDDRRDLDAERDRSLKSPMSRDSPLSKFKPLDSRNSRSKSLAS 167
QY 47 PANDPLVLLHSVSSLSELTELFCLGKRVKKRLERVOGGLDFSMLEQNDLEPG 106
DB 168 PTW-----SKDSGSEQSK---SVGNVKKSEEVQCKSSTTSSEMEGELEPE 212
QY 107 HTLELLASLRHDL-----RVVD-DF-EAGAAAGAAGEEDLCAAFVIC 153

DB 213 PQPETASGLAHQTKHKCKLPSCSADHKNAIDRSFOEIGKSA-----QLDANTESNREL 267
QY 154 DVGCDWRRLAROLKVSPTKID--STEDRIPKRLTERVRESLRIMKTEKENATVA---- 207
DB 268 SHVGGN-----REMETTDSMTDKSYED--AENVPEHAESMHSVSONNNDSTALAIER 320
QY 208 -HLVGALRSCOMNLVADLYOE 227
DB 321 DHRDGTI-TASANKITDLYDE 340

Search completed: June 19, 2003, 10:39:08
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:29:05 ; Search time 22 seconds

(Without alignments)
482,634 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNQAPRCRGGGILPLGRR.....RSGAMSPWNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1040	79.9	208	1 FADD_HUMAN
2	719.5	55.3	205	1 FADD_MOUSE
3	122	9.4	479	1 ICEB_HUMAN
4	121.5	9.3	1880	1 ANK1_HUMAN
5	117.5	9.0	1862	1 ANK1_MOUSE
6	115.5	8.9	656	1 RIK1_MOUSE
7	111.5	8.6	671	1 RIK1_HUMAN
8	110	8.4	480	1 CEFA_HUMAN
9	108	8.3	521	1 ICEA_HUMAN
10	99	7.6	3924	1 ANK2_HUMAN
11	98.5	7.6	4644	1 DYHC_MOUSE
12	98.5	7.6	4644	1 DYHC_RAT
13	96.5	7.4	535	1 HTR1_HUMAN
14	95.5	7.3	497	1 RP54_PSEAE
15	93.5	7.2	324	1 TNFR6_RAT
16	92	7.1	381	1 TNFR6_MOUSE
17	91.5	7.0	470	1 ANLY_MOUSE
18	91.5	7.0	1816	1 LMA4_HUMAN
19	91	7.0	3695	1 LMA4_MOUSE
20	90.5	7.0	130	1 PE15_MOUSE
21	90.5	7.0	411	1 RIK1_MOUSE
22	90	6.9	295	1 X769_HUMAN
23	90	6.9	953	1 YAA2_HUMAN
24	89.5	6.9	535	1 HTR1_HUMAN
25	89.5	6.9	429	1 AS10_HUMAN
26	89	6.8	483	1 RIK1_MOUSE
27	89	6.8	130	1 PE15_MOUSE
28	88.5	6.8	892	1 ANK1_HUMAN
29	88.5	6.8	893	1 ANK1_MOUSE
30	87.5	6.7	433	1 CBG1_HUMAN
31	87.5	6.7	484	1 CBG1_MOUSE
32	87.5	6.7	759	1 EPL1_HUMAN
33	87.5	6.7	759	1 EPL1_MOUSE

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	208 AA
34	FADD_HUMAN	013158: 014866;			
35	FADD_HUMAN	01-NOV-1997 (Rel. 35, Last sequence update)			
36	FADD_HUMAN	16-OCT-2001 (Rel. 40, Last annotation update)			
37	FADD_HUMAN	FADD protein (Fas-associated death domain-containing protein)			
38	FADD_HUMAN	(Mediator of receptor induced toxicity)			
39	FADD_HUMAN	FADD OR MORT1			
40	FADD_HUMAN	Homo sapiens (Human)			
41	FADD_HUMAN	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
42	FADD_HUMAN	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
43	FADD_HUMAN	NCBI_TaxID=9606;			
44	FADD_HUMAN	SEQUENCE FROM N.A. AND MUTAGENESIS.			
45	FADD_HUMAN	TISSUE=umbilical vein endothelial cells;			
		MEDLINE=95277837; PubMed=7538907;			
		Chinnaiyan A.M., O'Rourke K., Dixit V.M.;			
		"FADD", a novel death domain-containing protein, interacts with the			
		death domain of Fas and initiates apoptosis.";			
		Cell 81:505-512(1995).			
		[2]			
		SEQUENCE FROM N.A.			
		MEDLINE=95229578; PubMed=7536190;			
		Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,			
		Wallach D.;			
		"A novel protein that interacts with the death domain of Fas/Apo1			
		contains a sequence motif related to the death domain.";			
		J. Biol. Chem. 270:7795-7798(1995).			
		[3]			
		SEQUENCE FROM N.A.			
		TISSUE=Lung;			
		Strausberg R.;			
		Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
		[4]			
		STRUCTURE BY NMR OF 1-83.			
		MEDLINE=98241233; PubMed=9582077;			
		Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,			
		Leonard M.J., Feix S.W.;			
		"NMR structure and mutagenesis of the FADD (Mort1) death-effector			
		domain.";			
		Nature 392:941-945(1998).			
		[5]			
		FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR			
		CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE			
		RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX			
		(DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8			
		INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC			
		CYSTINE PROTEASES) MEDIATING APOPTOSIS.			
		[6]			
		SUBUNIT: INTERACTS WITH CEFA.			
		FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.			
		DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE			
		CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.			
		[7]			
		SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).			
		[8]			
		SIMILARITY: CONTAINS 1 DEATH DOMAIN.			


```

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CC -----
DR EMBL: U24231; AAA86517.1; -
DR EMBL: X84709; CA59197.1; -
DR EMBL: BC000334; AA000334.1; -
DR PDB: 1A1W; 16-FEB-99.
DR PDB: 1A1Z; 16-FEB-99.
DR Genew: HGNC:3573; FADD.
DR MIM: 602457; -
DR InterPro: IPR001875; DED.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
DR Pfam: PF01335; DED; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00031; DED; 1.
DR PROSITE: PSS0017; DEATH_DOMAIN; 1.
DR PROSITE: PSS0168; DED; 1.
DR Apoptosis; 3D-structure.
KW Apoptosis; 3D-structure.
FT DOMAIN 97 81 DED.
FT NOTAGN 121 121 V->N: NO INTERACTION WITH FAS RECEPTOR.
FT CONFLICT 32 32 G->V (IN REF. 2).
SQ SEQUENCE 208 AA; 23279 MW; 0E5E2F852E83507 CRC64;

Query Match
Best Local Similarity 99.5%; Score 1040; DB 1; Length 208;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPEVLVLSVSSSSSELTETKFLGKRVYRKLERVSGDLFSLMEQNDLEPGRHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFLGKRVYRKLERVSGDLFSLMEQNDLEPGRHT 60
QY 109 ELIRELLASLRHDLRRVDFEAGAAAGAPGEDICAFNVICDVGDMRLAROLK 168
DB 61 ELIRELLASLRHDLRRVDFEAGAAAGAPGEDICAFNVICDVGDMRLAROLK 120
QY 169 VSDTKIDSIEDRYPRNTERVERSLRTWKTEKENATVAHLYGALRSCQNLVADLYOEY 228
DB 121 VSDTKIDSIEDRYPRNTERVERSLRTWKTEKENATVAHLYGALRSCQNLVADLYOEY 180
QY 229 QOARDLONRSGAMSPMSWNSDASTSEAS 256
DB 181 QOARDLONRSGAMSPMSWNSDASTSEAS 208

RESULT 2
FADD_MOUSE STANDARD; PRT; 205 AA.
ID FADD_MOUSE 061160;
AC 061160; 061082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (Fas-associated death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MORT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96220459; Pubmed=8649383;
RA Zhang J., Minoto A.;
RT "A mouse Fas-associated protein with homology to the human MORT1/FADD
RT protein is essential for Fas-induced apoptosis.";
RL Mol. Cell. Biol. 16: 2756-2763(1996).

```

```

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96152659; Pubmed=8565075;
RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
RT "TRADD, TRAF2 and TRADD-FADD interactions define two distinct TNF
RT receptor 1 signal transduction pathways.";
RL Cell 84:299-308(1996).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (BY SIMILARITY).
CC Cysteine proteases) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH RECEPTOR DOMAIN (DED).
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CC -----
DR EMBL: U50406; AAB07789.1; -
DR EMBL: U43184; AAA97876.1; -
DR HSSP: Q13158; 1A1Z.
DR MGD: MGI:109324; Fadd.
DR InterPro: IPR001875; DED.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
DR Pfam: PF01335; DED; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00031; DED; 1.
DR PROSITE: PSS0017; DEATH_DOMAIN; 1.
DR PROSITE: PSS0168; DED; 1.
DR Apoptosis; 3D-structure.
KW Apoptosis; 3D-structure.
FT DOMAIN 97 81 DED.
FT NOTAGN 168 168 C->F (IN REF. 2).
FT CONFLICT 168 168 C->F (IN REF. 2).
SQ SEQUENCE 205 AA; 22960 MW; 4BC8D8533A58783 CRC64;

Query Match
Best Local Similarity 55.3%; Score 719.5; DB 1; Length 205;
Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

QY 49 MDPEVLVLSVSSSSSELTETKFLGKRVYRKLERVSGDLFSLMEQNDLEPGRHT 108
DB 1 MDPEVLVLSVSSSSSELTETKFLGKRVYRKLERVSGDLFSLMEQNDLEPGRHT 60
QY 109 ELIRELLASLRHDLRRVDFEAGAAAGAPGEDICAFNVICDVGDMRLAROLK 168
DB 61 ELIRELLASLRHDLRRVDFEAGAAAGAPGEDICAFNVICDVGDMRLAROLK 120
QY 169 VSDTKIDSIEDRYPRNTERVERSLRTWKTEKENATVAHLYGALRSCQNLVADLYOEY 228
DB 121 VSDTKIDSIEDRYPRNTERVERSLRTWKTEKENATVAHLYGALRSCQNLVADLYOEY 180
QY 229 QOARDLONRSGAMSPMSWNSDASTSE 254
DB 181 QES---VSKSNMSPVLRDSTVSSSE 203

RESULT 3
ICE8_HUMAN STANDARD; PRT; 479 AA.
ID ICE8_HUMAN 014790;
AC 014790; 014791; 014792; 014793; 014794; 014795; 014796; 015780;
AC 015806; 09U081; 014676;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CAP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Thymus, and B-cell;
RX MEDLINE=96279827; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Golitssev Y.V., Wallach D.,
RT Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/APO-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815(1996).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377;
RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Nij J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Kramer P.H., Peter M.E., Dixit V.M.;
RT FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
RL Cell 85:817-827(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Filtz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Tetzl T., Mel T., Valentine V., Kidd V.J.;
RT Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
RX MEDLINE=97373533; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., Ottilie S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545(1997).
RN [6]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
RN [7]
RP FUNCTION.
RX MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956(1997).
RN [8]
RP PROCESSING.
RX MEDLINE=97373557; PubMed=9184224;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.E.;
RT FLICE is activated by association with the CD95 death-inducing

RT signaling complex (DISC).";
RL EMBL J. 16:2794-2804(1997).
RN [9]
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RP MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Grutter M.G.;
RT The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133(1999).
CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
CC TNFR-1 INDUCED CELL DEATH. BINDING TO THE APOFOR MOLECULE FADD
CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED
CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC
CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.
CC CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY
CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-
CC MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-1-AMC. LIKELY TARGET FOR
CC THE COMPOX VIRUS CRMA DEATH INHIBITORY PROTEIN.
CC -1- SUBUNIT: HETERODIMER OF A 18 KDA (P18) AND A 10 KDA (P10) SUBUNIT.
CC INTERACTS WITH CELAR.
CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1-ALPHA (SHOWN HERE), 2-
CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-
CC BETA. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A
CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD
CC LEUCOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,
CC TESTIS, AND SKELETAL MUSCLE.
CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE
CC DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE
CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND
CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X98172; CAA66853.1; -
CC EMBL: X98173; CAA66854.1; -
CC EMBL: X98174; CAA66855.1; -
CC EMBL: X98175; CAA66856.1; -
CC EMBL: X98176; CAA66857.1; -
CC EMBL: X98177; CAA66858.1; -
CC EMBL: X98178; CAA66859.1; -
CC EMBL: U58143; AAC50602.1; -
CC EMBL: U60520; AAC50645.1; -
CC EMBL: AF102146; AAD24962.1; -
CC EMBL: AF102139; AAD24962.1; JOINED.
CC EMBL: AF102140; AAD24962.1; JOINED.
CC EMBL: AF102141; AAD24962.1; JOINED.
CC EMBL: AF102142; AAD24962.1; JOINED.
CC EMBL: AF102143; AAD24962.1; JOINED.
CC EMBL: AF102144; AAD24962.1; JOINED.
CC EMBL: AF102145; AAD24962.1; JOINED.
CC EMBL: AF009620; AAB70913.1; -
CC PDB: 1ODU; 1O-JUL-00.
CC MEROPS: C14-009; -
CC GeneW: HGNC:1509; CASP8.
CC MIM: 601763; -
CC InterPro: IPR001875; DED.
CC InterPro: IPR002138; ICE_P10.
CC InterPro: IPR001309; ICE_P20.

DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR Pfam; PF01335; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;
 KW Repeat; 3D-structure.
 FT PROPEP 1 216
 FT CHAIN 217 374 CASPASE-8 SUBUNIT P18.
 FT PROPEP 375 384
 FT CHAIN 385 479 CASPASE-8 SUBUNIT P10.
 FT ACT_SITE 317 317
 FT ACT_SITE 360 360
 FT DOMAIN 2 80
 FT DOMAIN 100 177
 FT VASPLIC 102 102
 FT VASPLIC 184 198
 FT VASPLIC 184 220
 FT VASPLIC 184 267
 FT VASPLIC 199 235
 FT VASPLIC 221 479
 FT VASPLIC 236 479
 FT VASPLIC 269 276
 FT VASPLIC 277 479
 FT CONFLICT 285 285
 FT CONFLICT 294 294
 FT CONFLICT 331 331
 FT SEQUENCE 479 AA; 55391 MW; 7A5FEA6B39B582P CRC64;
 Query Match 9.4%; Score 122; DB 1; Length 479;
 Best Local Similarity 28.8%; Pred. No. 0.025;
 Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;
 Oy 56 LHSVSSLSSELTSLKFLGKRVKRLERVGSLDFSLMLLEQNDLPCHTELLRELL 115
 Db 7 LYDGEQLDSEDLASLKLFLDYIPORKEPIKDALMFLQERKMLEESNLSEKLELL 66
 Oy 116 ASLRHLL-----RYDDFAGAGAAAGPEEDLCAFNYICNVGDMRR-----L 163
 Db 67 FRIRRLDLITYLNTREMEREL--QTGPAQI-SAYRVMLYQISEVSRSSELSRPF 122
 Oy 164 AROLKVSPTKID 175
 Db 123 LLOEISKCKID 134
 RESULT 4
 ID ANKI_HUMAN STANDARD: PRT: 1880 AA.
 AC P16157;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).
 GN ANKI OR ANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
 RC TISSUE=Hematopoietic;

RX MEDLINE-90158830; PubMed-2137557;
 RA Lux S.E., John K.M., Bennett V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 structure with homology to tissue-differentiation and cell-cycle
 control proteins.";
 RT Nature 344:36-42(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90175370; PubMed-1689849;
 RA Lambert S., Yu H., Pichal J.T., Lawler J., Ruff P., Spelcher D.,
 RA Cheung M.C., Kan Y.W., Palek J.;
 RT "cDNA sequence for human erythrocyte ankyrin.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
 RL [3]
 RP VARIANT HS ILE-462.
 RX MEDLINE-96225450; PubMed-8640229;
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 RA Dornwell M., Hebers J., Kugler W., Oezcan R., Pekrun A.,
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive
 hereditary spherocytosis.";
 RT Nat. Genet. 13:214-218(1996).
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
 CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
 PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1/2.1 (shown here),
 2/2.2 and 3; are produced by alternative splicing.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.
 CC -1- PTM: ACTIVATED BY PALMITIC ACID GROUP(S).
 CC -1- DISEASE: Defects in ANKI are the cause of dominant and recessive
 hereditary spherocytosis (HS).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X16609; CA34610.1; -;
 DR EMBL; M28880; AA51732.1; -;
 DR PIR; S08275; SJHOK.
 DR PIR; A35049; A35049.
 DR HSSP; 000420; IAWC.
 DR Genew; HGNC:492; ANKI.
 DR MIM; 182900; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 22.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.
 DR PROSITE; PS50086; ANK_REPEAT; 20.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;
 KW Polymorphism.
 FT INIT_MET 0 0
 FT DOMAIN 1 826 89 KDA DOMAIN (ANION EXCHANGE PROTEIN

Query Match	Best Similarity	9.3%: Score 121.51; DB 1; Length 1880;
Matches 34; Conservative	27.28; Pred. No. 0.15;	
	28; Mismatches 56; Indels 7; Gaps 2;	
QY 137 GAAPGEEIDICAFNYICDVGKDWDRRLAROLKVSPTKIDSIEDRYPNILTERVRESLRIV	1394 GSLSSTEQAEKMKMAYISHLGLSMELRLRELQFVEDINRIKRVENPNLSLBSVALNLIM	1453
DB 137 KNTKEKNAIVAHVLVALSKSCOMNLVADLYQ-EVQQAQRLQ-----NRSGAMSPKSNWSD	1454 VTRCOONNMENLYLALQSIDRGELVNNLSESGRQSRNLKDPDRRHTDSDYLSLSPQONGY	1513
QY 250 ASTSE 254		
DB 1514 SSLOD 1518		

RESULT 5	ID	ANK1_MOUSE	STANDARD:	PRT: 1862 AA.
AC	002357	ANK1_MOUSE		
DT	01-NOV-1995	(Rel. 32, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Ankyrin 1 (Erythrocyte ankyrin).			
DE	ANK1 OR ANK-1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=Erythrocyte;			
EX	MEDLINE=92345717; PubMed=1386265;			
RA	White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;			
RT	"Murine erythrocyte ankyrin cDNA: highly conserved regions of the regulatory domain."			
RL	Mamm. genome 3:281-285(1992).			
CC	-1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.			
CC	ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOSOLIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.			
CC	-1- SUBCELLULAR LOCATION: CYTOSOLIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.			
CC	-1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 23 ANK REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL: M84756; AAA37236.1; -			
DR	HSSP: 000420; IAWC.			
DR	MGI: MGI:88024; Ank1.			
DR	InterPro: IPR002110; ANK.			
DR	InterPro: IPR000488; Death.			
DR	InterPro: IPR00506; Z05.			
DR	Pfam: PF00023; ank; 24.			
DR	Pfam: PF00531; death; 1.			
DR	Pfam: PF00791; z05; 1.			
DR	PRINTS: PRO1415; ANKYRIN.			
DR	SMART: SM00248; ANK; 22.			
DR	SMART: SM00218; Z05; 1.			
DR	PROSITE: PS50088; ANK_REPEAT; 20.			
DR	PROSITE: PS50297; ANK_REPEAT; 1.			
DR	PROSITE: PS50107; DEATH_DOMAIN; 1.			
KW	Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.			
FT	DOMAIN 1 827			
FT	DOMAIN 828 1386			
FT	DOMAIN 1387 1862			
FT	REPEAT 40 69			
FT	REPEAT 73 102			
FT	REPEAT 106 135			
FT	REPEAT 139 168			
FT	REPEAT 170 197			
FT	REPEAT			

FT REPEAT 201 230 ANK 6.
 FT REPEAT 224 263 ANK 7.
 FT REPEAT 267 296 ANK 8.
 FT REPEAT 300 329 ANK 9.
 FT REPEAT 333 362 ANK 10.
 FT REPEAT 366 395 ANK 11.
 FT REPEAT 399 428 ANK 12.
 FT REPEAT 432 461 ANK 13.
 FT REPEAT 465 494 ANK 14.
 FT REPEAT 498 527 ANK 15.
 FT REPEAT 531 560 ANK 16.
 FT REPEAT 564 593 ANK 17.
 FT REPEAT 597 626 ANK 18.
 FT REPEAT 630 659 ANK 19.
 FT REPEAT 663 692 ANK 20.
 FT REPEAT 696 725 ANK 21.
 FT REPEAT 729 758 ANK 22.
 FT REPEAT 791 820 ANK 23.
 FT DOMAIN 1399 1483 DEATH.
 SQ SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001B5 CRC64;

Query Match 9.0%; Score 117.5; DB 1; Length 1862;
 Best Local Similarity 27.9%; Pred. No. 0.3;
 Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;

DB 151 VICDNVGMKWRRLARQLKVDKIDRIEDRYPRNLTREVRSLRINKTEKENATVAHLY 210
 1405 VIREHGLSMALRELCFSEVDINIRVENPNSLIDOSTALTTLWDRGENAKKENLY 1464
 QY 211 GALSQNMVLVDLVO-EVOQARDQ-----NRSGAMSPMSNDASTSE 254
 DB 1465 TALNRIDREIYNMELGSGRSHNKPERRHGDREYSLSPQVNGYSSLD 1515

RESULT 6

R1KLMOUSE
 ID R1KLMOUSE STANDARD; PRT; 656 AA.

AC 060855;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.1-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIPK1 OR RIP OR R1P.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT "RIP: a novel protein containing a death domain that interacts with
 Fas/PO-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
 INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-
 DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 CC -1- TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 or send an email to license@ebi.ac.uk).
 CC EMBL: U25995; AAB60487.1; -

DR HSP: P25445; 1DDF.
 DR MGD; MG1:108212; RipK1.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR pfam: PF00069; pkinase; 1.
 DR pfam: PF00531; death; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW Apoptosis.
 FT DOMAIN 17 290 PROTEIN KINASE.
 FT NP_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 568 654 DEATH.
 FT VARIANT 473 473 T->I.
 SQ SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;

Query Match 8.9%; Score 115.5; DB 1; Length 656;
 Best Local Similarity 34.9%; Pred. No. 0.12; 29; Indels 3; Gaps 3;
 Matches 29; Conservative 22; Mismatches 29;

QY 150 NVICDNVGMKWRRLARQLKVDKIDRIEDRYPRNLTREVRSLRINKTEKENATVA 207
 573 NPIREHGLSMALRELCFSEVDINIRVENPNSLIDOSTALTTLWDRGENAKKENLY 632
 DB 208 HLYGAL-RSQNMVLVDLVOEQ 229
 QY 633 KLAQALHCCCRIDLNLHLIRASQ 655

RESULT 7

R1KLHUMAN
 ID R1KLHUMAN STANDARD; PRT; 671 AA.

AC Q13546; Q13180;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.1-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIPK1 OR RIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=96200892; PubMed=8612133;
 RA Hsu H., Huang J., Shu H.-B., Balchwal V.R., Goeddel D.V.;
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
 receptor-1 signaling complex.";
 RL Immunity 4:387-396(1996).
 RN [2]
 RP REVISION TO 120.
 RA Huang J., Hsu H., Balchwal V.R., Goeddel D.V.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 300-671 FROM N.A.
 RC MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT "RIP: a novel protein containing a death domain that interacts with
 Fas/PO-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
 INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-

DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 - SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL; U50062; AAC3232.1; -
 DR HSP; U25994; AAC50137.1; -
 DR HSP; P08631; IAD5; -
 DR Genew; HENC110019; RIKP1.
 DR MIM; 603453; -
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00531; death; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KM Transerferase; Serine/threonine-protein kinase; ATP-binding;
 KM Apoptosis.

DOMAIN 17 269 PROTEIN KINASE.
 FT NF_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 583 669 DEATH.
 FT DOMAIN 411 414 POLY-ARG.
 FT CONFLICT 514 514 T -> S (IN REF. 3).
 FT SEQUENCE 671 AA; 75958 MW; BADCAETET0456ABE CRC64;

Query Match 8.68; Score 111.5; DB 1; Length 671;
 Best Local Similarity 36.48; Pred. No. 0.25; Indels 3; Gaps 3;
 Matches 28; Conservative 19; Mismatches 27;

QY 152 ICDNNGKMRRLARQLVSPDKIDSIEDRPRN-LTERVESLRIWNTK-ENATVAHL 209
 DB 590 IREHLGKMKNCARLQFTQSQIDEDHYERDLKRYKQVOMLOKVMREGIKGATVGL 649
 QY 210 VGALRSC-QMNVADYD 225
 DB 650 AQAHLQCSRIDLSLI 666

RESULT 8
 CELA_HUMAN STANDARD; PRT; 480 AA.
 AC 015519; 015356; 015137; 060458; 043618; 016673; 043619; 043620;
 AC 014675; 060459; 014674; 090EW1; 015510; 015138;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
 DE Inhibitory protein) (C-FLIP) (Caspase-eight-related protein) (Casper)
 DE (Caspase-like apoptosis regulatory protein) (CIARP) (MACH-related
 DE Inducer of toxicity) (WRIT) (Caspase homolog) (CASH) (Inhibitor of
 DE FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
 DE (Usurpin)
 GN CELAR OR CLARP OR WRIT OR CASH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF
 RP TYR-360
 RC TISSUE-Embryonic Kidney, and Umbilical vein endothelial cells;
 RX MEDLINE-97352452; PubMed-9208847;
 RA Shu H.-B., Halpin D.R., Goeddel D.V.;
 RT "Casper is a FADD- and caspase-related inducer of apoptosis.";
 RL Immunity 6:751-763(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE-97470967; PubMed-932610;
 RA Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Task B.J.,
 RA Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;
 RT "WRIT, a novel death-effector domain-containing protein, interacts
 RT with caspases and BclXL and initiates cell death.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Peripheral blood lymphocytes;
 RX MEDLINE-97360133; PubMed-9217161;
 RA Immler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
 RA Bodmer J.-L., Schroeder M., Burns K., Mattmann C., Rimoldi D.,
 RA French L.E., Tschopp J.;
 RT "Inhibition of death receptor signals by cellular FLIP.";
 RL Nature 388:190-195(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF
 RP ASP-376.
 RC TISSUE-T-cell;
 RX MEDLINE-97373543; PubMed-9228018;
 RA Srikrishna S.M., Ahmad M., Ohtsuka S., Bullrich F., Banks S.,
 RA Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armstrong R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis.";
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE-97362203; PubMed-9211860;
 RA Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 RT CD-95-induced apoptosis.";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE-Kidney;
 RX MEDLINE-99218584; PubMed-10200473;
 RA Rasper D.M., Vallancourt J.P., Hadano S., Houtzager V.M., Selden I.,
 RA Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 RA Koop B.F., Peterson E., Thornderry N.A., Huang J., Macpherson D.P.,
 RA Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 RA Nicholson D.W.;
 RT "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 RT homologous that precludes caspase-8 recruitment and activation by the
 RT CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Skin fibroblast;
 RX MEDLINE-97426025; PubMed-9289491;
 RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 RA Brodianskii V.M., Wallach D.;
 RT "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Colon carcinoma;

RX MEDLINE-98021435; PubMed-9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CARD-8, a death effector domain-containing protein interacts with
 RT caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP MEDLINE-99098697; PubMed-9889531;
 RA Scifaldi C., Schmitz I., Kramer P.H., Peter M.E.;
 RT "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1548(1999).
 RN [12]
 RP MEDLINE-99244884; PubMed-10227994;
 RA Alleciras-Schmittich A., Griffith T.S., Lynch D.H., Paya C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 RT Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 CC -1- FUNCTION: APOPTOSIS REGULATOR PROTEIN WHICH MAY FUNCTION AS A
 CC CRUCIAL LINK BETWEEN CELL SURVIVAL AND CELL DEATH PATHWAYS IN
 CC MAMMALIAN CELLS. ACTS AS AN INHIBITOR OF TNFRSF6 MEDIATED
 CC APOPTOSIS. A PROTEOLYTIC FRAGMENT (P43) IS LIKELY RETAINED IN THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) THEREBY BLOCKING FURTHER
 CC RECRUITMENT AND PROCESSING OF CASPASE-8 AT THE COMPLEX. FULL
 CC LENGTH AND SHORTER ISOFORMS HAVE BEEN SHOWN EITHER TO INDUCE
 CC APOPTOSIS OR TO REDUCE TNFRSF6-TRIGGERED APOPTOSIS. LACKS ENZYMATIC
 CC (CASPASE) ACTIVITY.
 CC -1- SUBUNIT: TNFRSF6 STIMULATION TRIGGERS RECRUITMENT TO THE DEATH-
 CC INDUCING SIGNALING COMPLEX (DISC) FORMED BY TNFRSF6, FADD AND
 CC CASPASE-8. A PROTEOLYTIC FRAGMENT (P43) STAYS ASSOCIATED WITH THE
 CC DISC. ALSO INTERACTS WITH CASPASE-10, CASPASE-3, TRAF1, TRAF2 AND
 CC BCL-X(L) (IN VITRO).
 CC -1- ALTERNATIVE PRODUCTS: 14 ISOFORMS: 1/FLIP-L/CARD1/WRIT ALPHA-
 CC 1/CASH ALPHA/FLIP-1/FLAME-1 GAMMA/USURPIN ALPHA (SHOWN HERE),
 CC 2/FLIP-S/CARD2/WRIT BETA-1/CASH BETA, 3/WRIT ALPHA-2, 4/T-FLICE
 CC 9, 5/T-FLICE 3, 6/T-FLICE 4, 7/T-FLICE 5, 8/FLAME-1 ALPHA,
 CC 9/FLAME-1 BETA, 10/FLAME-1 DELTA, 11/USURPIN BETA, 12/USURPIN
 CC GAMMA, 13 AND 14; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN
 CC SKELETAL MUSCLE, PANCREAS, HEART, KIDNEY, PLACENTA, AND PERIPHERAL
 CC BLOOD LEUKOCYTES. ALSO DETECTED IN DIVERSE CELL LINES. ISOFORM
 CC 8 IS PREDOMINANTLY EXPRESSED IN TESTIS AND SKELETAL MUSCLE.
 CC -1- INDUCTION: REPRRESSED BY IL-2 AFTER TCR STIMULATION, DURING
 CC PROGRESSION TO THE S-PHASE OF THE CELL CYCLE.
 CC -1- DOMAIN: THE CASPASE DOMAIN LACKS THE ACTIVE SITES RESIDUES
 CC INVOLVED IN CATALYSIS.
 CC -1- PM: PROTEOLYTICALLY PROCESSED: PROBABLY BY CASPASE-8. PROCESSING
 CC LATELY OCCURS AT THE DISC. GENERATES SUBUNIT P43 AND P12.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
 CC -----
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 CC -----
 CC EMBL AF010127; AAB64110.1;
 CC EMBL U85059; AAB82448.1;
 CC EMBL U97074; AAC51622.1;
 CC EMBL U97075; AAC51623.1;
 CC EMBL AF009617; AAB70912.1;
 CC EMBL AF009619; AAB70910.1;
 CC EMBL AF009616; AAB70909.1;
 CC EMBL AF009618; AAB70911.1;
 CC EMBL AF041458; AAB99790.1;

DR EMBL AF041459; AAB99791.1;
 DR EMBL AF041462; AAB99794.1;
 DR EMBL AF041461; AAB99793.1;
 DR EMBL AF041460; AAB99792.1;
 DR EMBL AF015452; AAC16441.1;
 DR EMBL AF015450; AAC16443.1;
 DR EMBL AF015451; AAC16440.1;
 DR EMBL Y14040; CAAT4367.1;
 DR EMBL Y14039; CAAT4366.1;
 DR EMBL AF005775; AAC15826.1;
 DR EMBL AF005774; AAC15825.1;
 DR EMBL BC001602; AAH01602.1;
 DR MEROPS C14.971;
 DR Genew; HGNC:1876; CFLAR.
 DR MIM; 603599;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00656; ICE_P20; 1.
 DR Pfam; PF01335; DED 2.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 KW Apoptosis; Repeat; 376
 FT CHAIN 1
 FT CHAIN 377 480
 FT 1 73
 FT DOMAIN 92 170
 FT 263 358
 FT DOMAIN 1 435
 FT 1 305
 FT DOMAIN 1 227
 FT 1 195
 FT DOMAIN 192 435
 FT 192 480
 FT DOMAIN 217 480
 FT 10..
 Query Match 8.4%; Score 110; DB 1; Length 480;
 Best Local Similarity 25.9%; Pred. No. 0.22;
 Matches 49; Conservative 29; Mismatches 93; Indels 18; Gaps 6;
 QY 55 LHSVSSLSSELTFLKFLGRVYKRLERVOGDLFMSLLEONLPGHTELLNEL 114
 DB 5 VHOVEALDDEKEMFLFLCDVAIDVPPVPR---DLDLIRKGLSTGD---LDEL 58
 QY 115 LASLRHDLRLRYDDFEAGAAAGPGEEDICAFNVICDVGKDWRIARQLKVDK 173
 DB 59 LYRVARFDLKRILKMDKRAVETHLRNPHLYSDRVLMAEIGD-----LDRSDVSS 111
 QY 174 -IDSIEDRYPRRLTRVRESIRIKNTKEKNAVHVLGALRSQGNL-VADIVGNOQA 231
 DB 112 LIFLRKDYMGKRIKRSKSPFLDLVELEKLVAVAPDQLLEKCKLNIRIDLTXTIOKY 171
 QY 232 RDLQNRSGA 240
 DB 172 K--GSVQQA 178
 RESULT 9
 ID ICEA HUMAN STANDARD: PRT; 521 AA.
 AC 092851; 099845; 091206; 091207;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 4)
 DE (Apoptotic protease Mch-4) (Fas-associated death domain protein
 DE Interleukin-18-converting enzyme 2) (FLICE2).
 DE CASP10 OR MCH4.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_Taxid=9606;
 CC [1]
 CC SEQUENCE FROM N.A. (ISOFORM A).
 CC TISSUE=T-cell;
 CC MEDLINE=96353638; PubMed=8755496;
 CC Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 CC Wang L., Bullrich F., Fritz L.C., Trappant J.A., Tomaselli K.J.,
 CC Litwack G., Alnemri E.S.;
 CC "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 CC apoptotic cysteine protease containing two FAD-like domains.";
 CC Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORM B).
 CC MEDLINE=97197836; PubMed=9045686;
 CC Vincenz C., Dixit V.M.;
 CC "Fas-associated death domain protein interleukin-1beta-converting
 CC enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
 CC CD95- and p55-mediated death signaling.";
 CC J. Biol. Chem. 272:6578-6583(1997).
 CC [3]
 CC SEQUENCE FROM N.A. (ISOFORMS B AND C).
 CC TISSUE=Thymus, and Spleen;
 CC MEDLINE=99214592; PubMed=10187817;
 CC Ng P.W., Porter A.G., Janicke R.U.;
 CC "Molecular cloning and characterization of two novel pro-apoptotic
 CC isoforms of caspase-10.";
 CC J. Biol. Chem. 274:10301-10308(1999).
 CC [4]
 CC SEQUENCE FROM N.A. (ISOFORM A).
 CC MEDLINE=21100893; PubMed=11161814;
 CC Hadano S., Yanagisawa Y., Skaug J., Richter K., Nasir J.,
 CC Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 CC Ikeda J.-E., Hayden M.R.;
 CC "Cloning and characterization of three novel genes, A1S2CR1, A1S2CR2,
 CC and A1S2CR3, in the juvenile amyotrophic lateral sclerosis (A1S2)
 CC critical region at chromosome 2q33-q34: candidate genes for A1S2";
 CC Genomics 71:200-213(2001).
 CC [5]
 CC PARTIAL SEQUENCE, AND PROCESSING.
 CC MEDLINE=97121412; PubMed=8962078;
 CC Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
 CC Alnemri E.S.;
 CC "Molecular ordering of the Fas-apoptotic pathway: the Fas/Apo-1
 CC protease Mch5 is a Crma-inhibitable protease that activates multiple
 CC Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND
 CC TNFR-1 RECEPTORS IN A FADD DEPENDENT MANNER. MAY PARTICIPATE IN
 CC THE GRANZYME B APOPTOTIC PATHWAYS. CLEAVES AND ACTIVATES CASPASE-
 CC 3, -4, -6, -7, -8, AND -9. HYDROLYZES THE SMALL- MOLECULE
 CC SUBSTRATES: TIR-VAL-ALA-ASP-1-AMC AND ASP-GLU-VAL-ASP-1-AMC.
 CC -1- FUNCTION: ISOFORM C IS PROTEOLYTICALLY INACTIVE.
 CC -1- SUBUNIT: HETERODIMER OF A 23/17 kDa (P23/17) DEPENDING ON THE
 CC SPLICING EVENTS AND A 12 kDa (P12) SUBUNIT.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS, A/10-A (SHOWN HERE), B/10-B AND
 CC C/10-C ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION
 CC IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.
 CC -1- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
 CC THE TWO ACTIVE SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
 CC -----
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DR EMBL, U60519; AAC50644.1; -
 DR EMBL, U86214; AAB46730.1; -
 DR EMBL, AF111344; AAD28402.1; -
 DR EMBL, AF111345; AAD28403.1; -
 DR EMBL, AB038979; BAB32554.1; -
 DR EMBL, AB038973; BAB32554.1; JOINED.
 DR EMBL, AB038974; BAB32554.1; JOINED.
 DR EMBL, AB038975; BAB32554.1; JOINED.
 DR EMBL, AB038976; BAB32554.1; JOINED.
 DR EMBL, AB038977; BAB32554.1; JOINED.
 DR HSSP, Q15806; 10DDU.
 DR MEROPS, C14.011; -
 DR GeneW, HGNC:1500; CASP10.
 DR MIM, 601762; -
 DR InterPro, IPR001875; DED.
 DR InterPro, IPR002398; ICE.
 DR InterPro, IPR002138; ICE_p10.
 DR InterPro, IPR001309; ICE_p20.
 DR Pfam, PF00655; ICE_p10; 1.
 DR Pfam, PF00656; ICE_p20; 1.
 DR Pfam, PF01335; DED; 2.
 DR PRINTS, PR00376; ILIBENZYM.
 DR SMART, SM00115; CASC; 1.
 DR SMART, SM00031; DED; 2.
 DR PROSITE, PS01122; CASPASE_CYS; 1.
 DR PROSITE, PS01121; CASPASE_HIS; 1.
 DR PROSITE, PS50207; CASPASE_P10; 1.
 DR PROSITE, PS50208; CASPASE_P20; 1.
 DR PROSITE, PS50168; DED; 2.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat;
 KW Alternative splicing.
 KW PROPEP 1 219
 FT CHAIN 220 415 CASPASE-10 SUBUNIT P23/17.
 FT CHAIN 416 521 CASPASE-10 SUBUNIT P12.
 FT DOMAIN 19 97 DED 1.
 FT DOMAIN 114 187 DED 2.
 FT ACT_SITE 358 358 BY SIMILARITY.
 FT ACT_SITE 401 401 BY SIMILARITY.
 FT VARSPPLIC 229 271 MISSING (IN SHORT ISOFORM).
 FT VARSPPLIC 473 521
 FT FT
 FT VARSPPLIC 241 273
 FT FT
 FT VARSPPLIC 274 521
 FT CONFLICT 68 68 E -> G (IN REF. 2).
 FT CONFLICT 268 268 T -> A (IN REF. 3).
 FT CONFLICT 410 410 V -> I (IN REF. 3).
 SQ SEQUENCE 521 AA; 58950 MW; 840348AE602B8243 CRC64;
 Query Match 8.3%; Score 108; DB 1; Length 521;
 Best local Similarity 35.7%; Pred. No. 0.34;
 Matches 25; Conservative 15; Mismatches 30; Indels 0; Gaps 0;
 OY 59 VSSSSSSELTLEKFCIGRVYKRIKERVQSGDLFSMLKQNDLSPGTELLRELLAST 118
 DB 27 IDSNIGVDVENLKEFCIGLVENKLEKSSASDVFEHLADLSEDPFELAEILYII 86
 OY 119 RRDDLRLRYD 128
 DB 87 ROKKLLQHLN 96
 RESULT 10
 ANK2_HUMAN
 ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
 AC 001484; 001485;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythrocyte).
 GN ANK2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE-BRAIN stem; PubMed-1830053;
 RX MEDLINE-91302466; PubMed-1830053;
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RT "Isolation and characterization of cDNAs encoding human brain
 ankyrins reveal a family of alternatively spliced genes."
 RL J. Cell Biol. 114:241-253(1991).
 RN [2]
 RP REVISIONS.
 RA Carpenter S.;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-BRAIN stem; PubMed-8253844;
 RX MEDLINE-94075409; PubMed-8253844;
 RA Chan W., Kordell E., Bennett V.;
 RT "440-kD ankyrinB: structure of the major developmentally regulated
 domain and selective localization in unmyelinated axons."
 RL J. Cell Biol. 123:1463-1473(1993).
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE-92009921; PubMed-1833308;
 RA Tee W.T., Menninger J.C., Yang-Peng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 ankyrin gene."
 RL Genomics 10:858-866(1991).
 CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
 elements. Also bind to cytoskeletal proteins.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CELLS THROUGHOUT THE BRAIN.
 CC -1- PTM: PHOSPHORYLATION AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 AND FUNCTION (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC or send an email to license@sdb-sdb.ch).
 CC
 DR EMBL; X56957; CAA40278.1; -;
 DR EMBL; X56958; CAA40279.2; -;
 DR EMBL; Z26634; CAA42644.1; -;
 DR EMBL; M37123; AAF62828.1; -;
 DR PIR; S14533; S14533;
 DR PIR; A39643; A39643;
 DR PIR; B39643; B39643;
 DR PIR; S14569; S14569;
 DR HSP; P42771; IDC2.
 DR Gene; HGNC:493; ANK2.
 DR MIM; 106410; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR004088; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF00023; ank; 24
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.

DR PROSITE; PS50086; ANK_REPEAT; 20;
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation.
 FT REPEAT 63 92 ANK 1.
 FT REPEAT 96 125 ANK 2.
 FT REPEAT 129 138 ANK 3.
 FT REPEAT 162 191 ANK 4.
 FT REPEAT 193 220 ANK 5.
 FT REPEAT 232 261 ANK 6.
 FT REPEAT 265 294 ANK 7.
 FT REPEAT 298 327 ANK 8.
 FT REPEAT 331 360 ANK 9.
 FT REPEAT 364 393 ANK 10.
 FT REPEAT 397 426 ANK 11.
 FT REPEAT 430 459 ANK 12.
 FT REPEAT 463 492 ANK 13.
 FT REPEAT 496 525 ANK 14.
 FT REPEAT 529 558 ANK 15.
 FT REPEAT 562 591 ANK 16.
 FT REPEAT 595 624 ANK 17.
 FT REPEAT 628 657 ANK 18.
 FT REPEAT 661 690 ANK 19.
 FT REPEAT 694 723 ANK 20.
 FT REPEAT 727 756 ANK 21.
 FT REPEAT 760 789 ANK 22.
 FT REPEAT 793 822 ANK 23.
 FT DOMAIN 1773 1950 REPEAT -RICH REGION.
 FT REPEAT 1773 1784 REPEAT A.
 FT REPEAT 1785 1796 REPEAT A.
 FT REPEAT 1797 1808 REPEAT A.
 FT REPEAT 1809 1820 REPEAT A.
 FT REPEAT 1821 1832 REPEAT A.
 FT REPEAT 1833 1844 REPEAT A.
 FT REPEAT 1845 1856 REPEAT A.
 FT REPEAT 1857 1867 REPEAT A.
 FT REPEAT 1868 1879 REPEAT A.
 FT REPEAT 1880 1891 REPEAT A.
 FT REPEAT 1892 1902 REPEAT A (APPROXIMATE).
 FT REPEAT 1903 1914 REPEAT A.
 FT REPEAT 1915 1926 REPEAT A.
 FT REPEAT 1927 1938 REPEAT A.
 FT REPEAT 1939 1950 REPEAT A.
 FT DOMAIN 3536 3620 DEATH.
 FT VASPLIC 1039 1039 Q -> QFGKLTLPAPPLNGESLVSRIQLGPPGTR
 (IN ISOFORM 2).
 FT VASPLIC 1444 3528 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT CONFLICT 475 476 GO -> PE (IN REF. 4).
 FT CONFLICT 971 971 I -> S (IN REF. 1).
 FT CONFLICT 3581 3582 QY -> HA (IN REF. 1).
 FT CONFLICT 3586 3586 I -> Y (IN REF. 1).
 SQ SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;

Query Match 7.6%; Score 99; DB 1; Length 3924;
 Best Local Similarity 23.9%; Pred. No. 21;
 Matches 32; Conservative 25; Mismatches 59; Indels 18; Gaps 3;
 OY 123 LLRRVDEPAGAAAGPEED--LCAAFNYICDVGKDMRLAQLVSPDKIDSIDR 180
 DB 3513 LIERTPD-ENGHDHEDQDEDERIEERLAIYADHLGFSWELARELDTPEQIQINIE 3571
 OY 181 YPRNTERVRESLRITWKTERENATVAHLVGALRSCQNNLVADLVQ----- 226
 DB 3572 NPNSLDQSOYLTKITLREDKHATDTMLVDELTKINRMDIVHLMETPELOERISHSY 3631
 OY 227 -EVQARDLQNRSG 239
 DB 3632 AEIEQTITLDHSEG 3645

RESULT 11
 DYHC_MOOSE

```

Query Match 7.6%; Score 98.5; DB 1; Length 4644;
Best Local Similarity 23.5%; Pred. No. 28;
Matches 59; Conservative 32; Mismatches 83; Indels 77; Gaps 12.

OY 53 LVLLHSVSSLSSELTPLKFLGRRYKRLERYOSGL-----DL 93
Db 376 .LRLVEAISRLDLSOLLKLVGTRKLHVAEVEEFEMVACFEVFTWDEYERKLOVLLRDI 435
OY 94 FSMLEON-----DLEPGHTEL--LRELIALSRHHLLR--RVDDFEAGAAA---G 137
Db 436 VKRRREELKKWVRINPARRKRLQARLDQRRFRROHEQLRAIVIRLPQVTAVAQOQNG 495
OY 138 AAPGEDPCCA-----FNVCNV-----GKD-----WRRLARQLKYS D 171
Db 496 EAPRPQDKVAEVLFDADANTATIEVNLAYENKVAEYGLDVSKEGTEAME---AAMKRYD 552
OY 172 TKDISIEDRYRNRLTERRESRLRWKNT-----EKENATVA--HLVGALRSOMNTIYA 222

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DB	553	ERIDREVER-----ITARLRDGLGRKANKNEFRIFSRNALFVPHRNGALRXYQTOLIO	608
OY	223	DLYOEVQOARD	233
DB	609	RVKDDIELSHD	619
RESULT 12			
ID	DYHC_RAT	STANDARD:	PRT: 4644 AA.
AC	P38650; Q63178;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	16-FEB-1995 (Rel. 31, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy chain) (MAP 1C).		
GN	DNCH1 OR DNCH1 OR DNEC1 OR MAP1C.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Missat; TISSUE=Brain;		
RX	MEDLINE=93376715; PubMed=7690137;		
RA	Zhang Z., Tanaka Y., Nonaka S., Alzawa H., Kawasaki H., Nakata T., Hirokawa N.;		
RT	"The primary structure of rat brain (cytoplasmic) dynein heavy chain, a cytoplasmic motor enzyme.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 90:7928-7932(1993).		
RP	[2]		
RC	SEQUENCE FROM N.A.		
RX	STRAIN=Sprague-Dawley; TISSUE=Brain;		
RA	MEDLINE=93264075; PubMed=7684332;		
RA	Mikami A., Paschal B.M., Mazumdar M., Vallee R.B.;		
RT	"Molecular cloning of the retrograde transport motor cytoplasmic dynein (MAP 1C).";		
RL	Neuron 10:787-796(1993).		
CC	-1- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES.		
CC	-1- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL, D13896; BAA02996.1; -		
DR	EMBL, L08505; AAA41103.1; -		
DR	PIR: A38905; A38905.		
DR	InterPro: IPR004273; Dynein heavy.		
DR	Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.		
FT	DOMAIN	48	69
FT	DOMAIN	179	200
FT	DOMAIN	453	476
FT	DOMAIN	541	564
FT	DOMAIN	1169	1201
FT	DOMAIN	1229	1250
FT	DOMAIN	1355	1371
FT	DOMAIN	2012	2040
FT	DOMAIN	3187	3273
FT	DOMAIN	3394	3498
FT	DOMAIN	3735	3798
FT	NP_BIND	1904	1911
FT	NP_BIND	2222	2229
FT	NP_BIND	2222	2229

FT NE_BIND 2593 2600 ATP (POTENTIAL).
 FT NE_BIND 2935 2942 ATP (POTENTIAL).
 FT CONFLICT 1024 1025 SR -> MP (IN REF. 2).
 FT CONFLICT 1772 1772 N -> D (IN REF. 2).
 FT CONFLICT 2098 2098 P -> A (IN REF. 2).
 FT CONFLICT 2139 2139 F -> V (IN REF. 2).
 FT CONFLICT 2175 2175 D -> Q (IN REF. 2).
 FT CONFLICT 2185 2185 L -> V (IN REF. 2).
 FT CONFLICT 2366 2366 T -> S (IN REF. 2).
 FT CONFLICT 2382 2382 A -> D (IN REF. 2).
 FT CONFLICT 2463 2463 R -> K (IN REF. 2).
 FT CONFLICT 3219 3219 F -> S (IN REF. 2).
 FT CONFLICT 4131 4131 A -> G (IN REF. 2).
 FT CONFLICT 4366 4366
 FT CONFLICT 4511 4511
 SQ SEQUENCE 4644 AA; 532240 MM; 8C6ABDEBF875D82 CRC64;

 Query Match 7.68; Score 98.5; DB 1; Length 4644;
 Best Local Similarity 23.58; Pred. No. 28;
 Matches 59; Conservative 32; Mismatches 83; Indels 77; Gaps 12;

 QY 53 LVLLHSVSSLSSELTETELKFLCGRVKKRLERVOGSL-----DL 93
 DB 376 LRLVFAISRLSSQLKVLGTRKIMHYADEFERVMACEFVQTMDEYKQLVLRDI 435
 QY 94 FSMLEQN-----DLEPHTL---IRELLASLRHDLR---RVDFENGAAA---G 137
 DB 436 VKRRREENTLKMVRINPAHRLKARLDQMRFRHQHQLRAVIVLRPQVAVAOQNOG 495
 QY 138 AARGEDLCA-----FNVIDNV-----GRD-----WRRLAQQLVSD 171
 DB 496 EAPPOOMKAEVLEPDAADANAIEVNAVLENKVDGLVSKGTEAME---AAMRYD 552
 QY 172 TKIDSIDRYPRNTEREVSRLRIKNT-----ERENATVA---HLVGALRSCOMNIVA 222
 DB 553 ERIDRYETR---ITALRQOLGAKANAMERFRISFNLFPVRPHRGALREYQTOIQ 608
 QY 223 DLYOEVQOARD 233
 DB 609 RVKDDIESLHD 619

 RESULT 13
 HTR1_HALSA STANDARD; PRT; 535 AA.
 ID HTR1_HALSA
 AC P33955;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sensory rhodopsin I transducer (HTR-I) (Methyl-accepting phototaxis protein I) (MPP-I).
 GN HTR1 OR HTR1 OR HTR.
 OS Halobacterium salinarum.
 CC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
 CC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID-2242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-L33;
 RX MEDLINE-90384855; PubMed-2205842;
 RA Ferrando E., Kirsh M., Marwan W., Oesterhelt D.;
 RT "A gene from S. pombe with homology to E. coli RNase III blocks conjugation and sporulation when overexpressed in wild type cells";
 RL Nucleic Acids Res. 18:5304-5304(1990).
 RN [2]
 RP FUNCTION
 RX MEDLINE-94244615; PubMed-8187768;
 RA Kirsh M., Marwan W., Vermeglio A., Oesterhelt D.;
 RT "Phototaxis of Halobacterium salinarum requires a signalling complex of sensory rhodopsin I and its methyl-accepting transducer HtrI";
 RL EMO J. 13:2150-2155(1994).
 CC -1- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSOR RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO

CC -1- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
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 CC
 CC EMBL: X68591; CAA48578.1;
 DR PIR: S28466; S28466.
 DR HSSP: P02942; 1007.
 DR InterPro: IPR004089; Chmtaxis_transd.
 DR InterPro: IPR003650; HAMP.
 DR Pfam: PF00015; MCPsignal; 1.
 DR Pfam: PF00672; HAMP; 1.
 DR SMART: SM00304; HAMP; 2.
 DR SMART: SM00283; MA; 1.
 DR Transducer; Photoreceptor; Transmembrane; Methylation.
 KW INT_MET 0 8 BY SIMILARITY.
 FT TRANSMEM 1 9 POTENTIAL.
 FT DOMAIN 30 33 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 34 34 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 34 34 POTENTIAL.
 FT TRANSMEM 55 535 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 265 265 METHYLATION (BY SIMILARITY).
 FT MOD_RES 272 272 METHYLATION (BY SIMILARITY).
 FT MOD_RES 279 279 METHYLATION (BY SIMILARITY).
 FT MOD_RES 463 463 METHYLATION (BY SIMILARITY).
 FT MOD_RES 472 472 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 535 AA; 56814 MM; 504A1654A7FA8A5 CRC64;

 Query Match 7.48; Score 96.5; DB 1; Length 535;
 Best Local Similarity 23.68; Pred. No. 2.8;
 Matches 47; Conservative 37; Mismatches 64; Indels 51; Gaps 9;

 QY 88 QSGDLFSMLEONDLEPGHTELLRELLASLRHDLRVD-----FEAGA 134
 DB 292 KSALDEMSITEVEDDPVGVEHRLDQVAEIT--DIVDVTIDIEGTNMLNLSIEAAR 349
 QY 135 AAGAARPEEDICAFNVCNVDGMDRRLARQLKVSPTKIDSDRPRNTEREVSRL 193
 DB 350 AGGNADD-----GFSVADEV-RD---LAEETQDRANETAAVVEKTAQ--TEVYASIO 399
 QY 194 ----RIKNTKEKENATVAHLVGALRSCOMLVADVOEV-----QOARDLQNR 237
 DB 400 HTRIRVESGSTVYSTILHT-----RTINDSISEVNSIDEIGRTTSEGAETVOST 450
 QY 238 SGANSPMSWNSDASTSENS 256
 DB 451 ATSEYRVAGLSDDTTALAS 469

 RESULT 14
 RP54_PSEAE STANDARD; PRT; 497 AA.
 ID RP54_PSEAE
 AC P49988;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RNA polymerase sigma-54 factor.
 GN RPON OR PA4462.
 OS Pseudomonas aeruginosa.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID-287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PAK;
 RX MEDLINE-94156835; PubMed-8113171;
 RA Jin S., Ishimoto K., Lory S.;

FT	DISULEID	103	123	BY SIMILARITY.
FT	DISULEID	125	139	BY SIMILARITY.
FT	DISULEID	142	154	BY SIMILARITY.
FT	DISULEID	145	162	BY SIMILARITY.
FT	CARBOHYD	43	43	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	114	114	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	324 AA;	36835 MW;	D25D583C909D09 CRC64;

Query Match 7.2%; Score 93.5; DB 1; Length 324;
 Best Local Similarity 23.8%; Pred. No. 2.6;
 Matches 39; Conservative 26; Mismatches 68; Indels 31; Gaps 6;

OY	78	RVVKKRLERVOSGIDLFSLLEQNDLEPGTELLRELLASLRHDLRRVDDFEAGAAG	137
Db	156	RTSNTCKCKROSSNYKILMLL-----ILPG-----LAILFVFIYKRYRKRPQDPESG----	202
OY	138	AARGEDLCARFVYICDNYGK-----DMRLAQQLKYSQDKIDSIEDRYPRNL	185
Db	203	-IPSPESV--PMNVSDVNLNKYIWRTAERKKICDARKFARQHKIPESKIDIEHNSPDA	259
OY	186	TERVRESLRIMKTEKENATVAHLVGAIRSCQMLVADLVQEVQ	229
Db	260	AEQKIQLOQWYQSHGRTGACQALIGLRANR---CDIAEIQ	300

Search completed: June 19, 2003, 10:37:15
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:34:25 ; Search time 80 Seconds
(without alignments)
659.351 Million cell updates/sec

Title: US-09-933-814-2

Perfect score: 1302
Sequence: 1 VNGAECRFGGILPLGR.....RSGAMSPKSNNDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	716	55.0	208	11	08R2E7
2	131.5	10.1	482	11	09JHX4
3	128.5	9.9	476	13	0918J3
4	128	9.8	538	4	08RDI5
5	125.5	9.6	480	11	08RDI10
6	122.5	9.4	239	5	09V3B4
7	122	9.4	171	4	08RDI11
8	122	9.4	276	4	09GK22
9	122	9.4	339	4	08RDI3
10	122	9.4	353	4	08RDI2
11	121.5	9.3	1856	4	099407
12	119.5	9.2	418	13	08RDI5
13	118.5	9.1	1719	4	013768
14	118	9.1	941	11	061302
15	117.5	9.0	1848	11	061302
16	116.5	8.9	1975	5	09VCD1

17	116	8.9	93	4	08RDI4	08td14 homo sapien
18	116	8.9	496	4	09COK4	09COK4 homo sapien
19	111	8.5	482	13	09OWU1	09OWU1 gallus gall
20	110	8.4	462	4	09GTE4	09GTE4 homo sapien
21	109	8.4	520	13	09IB62	09IB62 xenopus lae
22	108	8.3	479	4	08RDI8	08RDI8 homo sapien
23	103.5	7.9	461	5	096407	096407 lltomospide
24	103.5	7.9	970	5	017342	017342 caenorhabd1
25	103.5	7.9	985	5	017341	017341 caenorhabd1
26	103.5	7.9	1786	5	017344	017344 caenorhabd1
27	103	7.9	1809	5	017487	017487 caenorhabd1
28	103	7.9	1815	5	017488	017488 caenorhabd1
29	103	7.9	1867	5	017485	017485 caenorhabd1
30	103	7.9	2039	5	017489	017489 caenorhabd1
31	103	7.9	6994	5	017343	017343 caenorhabd1
32	101.5	7.8	500	13	09IB64	09IB64 xenopus lae
33	100	7.7	2091	5	09V769	09V769 drosophila
34	99.5	7.6	218	11	09R2M5	09R2M5 rattus norv
35	99	7.6	919	16	09R2A6	09R2A6 pseudomonas
36	99	7.6	927	2	087015	087015 pseudomonas
37	99	7.6	1955	5	061308	061308 parascaris
38	98	7.5	472	10	09G3N5	09G3N5 oryza sativ
39	97	7.5	487	5	09G3M2	09G3M2 stivela clav
40	97	7.5	622	17	09RQ32	09RQ32 halobacteri
41	97	7.5	665	4	096M89	096M89 homo sapien
42	96.5	7.4	560	4	08RDI1	08RDI1 homo sapien
43	96.5	7.4	1162	10	09LY65	09LY65 arabidopsis
44	96	7.4	647	16	09HUB1	09HUB1 pseudomonas
45	95.5	7.3	509	16	09A2N4	09A2N4 caulobacter

ALIGNMENTS

RESULT 1

08R2E7 PRELIMINARY; PRT; 208 AA.

AC 08R2E7; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Fas death domain associated protein.

GN FADD.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_Taxid-10116;

RN [1]

RC SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-ISCHEMIC BRAIN;

RA Spadoni C.G.;

RT Identification of neuronal caspases and involvement of death domain

RT proteins in neuronal apoptosis.

RL Theiss (2001), University of London, London, United Kingdom.

DR EMBL; AJ441127; CAD29628.1; -

SQ SEQUENCE 208 AA; 23124 MW; ABA3305406137CDB CRC64;

Query Match 55.0%; Score 716; DB 11; Length 208;

Best local Similarity 68.9%; Pred. No. 1.2e-51;

Matches 142; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

QY	49	MDPEVLHSSVSSSSSELTEIKFYCLGRVYKRIKERVQSGIDLFMSLIDNDLEPGHT	108
DB	1	MDPEVLHSSVSSSSSELTEIKFYCLGRVYKRIKERVQSGIDLFMSLIDNDLEPGHT	60
QY	109	ELIRELLASLRHDLRLRVDDPEAGAAAGPEEDLCAPNYICNVKQWRRLAROK	168
DB	61	GLIRELLASLRHDLRLRVDDPEAGAAAGPEEDLCAPNYICNVKQWRRLAROK	120

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OY 169 VSDPKIDIEDRPNTLETERRESLRITKNTKENTATYAHVGLRSCOMLVADLVQEV 228
DB 121 VSEKIDIGIERRYSRSDRRETLRWKNEKENASVAGLVKALRACRLMVLADLVBEA 180
OY 229 QOARDLONRSGAMSPMSMNSDASTSE 254
DB 181 LMAOGSVSKSDDTSSALRDSIVSFSE 206

RESULT 2
O9JHX4 PRELIMINARY; PRT; 482 AA.
AC O9JHX4
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-8.
GN CASP8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Itch T., Itch A., Pleasure D.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-CEREBELLUM;
RA Cao G., Graham S.H., Chen D., Chen J.;
RT "Molecular cloning and characterization of rat caspase-8: its
RT implication in delayed neuronal cell death after ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279308; AAF87778.1;
DR EMBL; AF288372; AAK83055.1;
DR HSSP; Q15806; 10DU.
DR MEROPS; C14.009; -.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match 10.1%; Score 131.5; DB 11; Length 482;
Best Local Similarity 40.5%; Pred. No. 0.01;
Matches 32; Conservative 12; Mismatches 34; Indels 1; Gaps 1;

OY 49 MDPFLVILHSVSSLSSELTFLKFLCGRYVKKRLLEVQGLDFFSLMLBQNDLEPGHT 108
DB 1 MD-PRSCYDIAERLGNELALAKFLCDHPKQESINDVLYLFQRLQEGMLEEDNL 59
OY 109 ELRELASLRHDLRRV 127
DB 60 SELKELFHISRDLRSRV 78

RESULT 3
O9IBJ3 PRELIMINARY; PRT; 476 AA.
AC O9IBJ3
ID O9IBJ3
RX O9IBJ3;
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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-8.
GN CASP8.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF273220; AAF79207.1;
DR HSSP; Q15806; 10DU.
DR MEROPS; C14.009; -.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50168; DED; 2.
SQ SEQUENCE 476 AA; 54890 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match 9.9%; Score 128.5; DB 13; Length 476;
Best Local Similarity 28.1%; Pred. No. 0.018;
Matches 59; Conservative 29; Mismatches 83; Indels 39; Gaps 10;

OY 49 MDPFLVILHSVSSLSSELTFLKFLCGRYVKKRLLEVQGLDFFSLMLBQNDLEPGHT 108
DB 1 MD-PRSCYDIAERLGNELALAKFLCDHPKQESINDVLYLFQRLQEGMLEEDNL 55
OY 109 ELRELASLRHDLRRVDFEAGAAAGAPGEDICAAFNVCNVAGD---WRRLA 164
DB 56 ELLEPELLIAIGRIDLLEILKSKREV-----ERNL-----LNCDSRGSAYRRML 103
OY 165 ROLKSDPKIDIEDR-----PNTLETERRESLRITKNTKENTATYAHVGL 211
DB 104 -LKISE--DWTENFPAKFLDLPRAKIGRSISFDALILEMKQRLPNDLELYR 158
OY 212 ALRSCOMLVADLVQEVQOARDLONRSGAM 241
DB 159 ILKCDKQLAWIERFRQSHNDQGGRL 188

RESULT 4
O8TD15 PRELIMINARY; PRT; 538 AA.
AC O8TD15
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Procaspase-8L.
GN CASP8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-21927603; PubMed-11917123;
```

RA Breckenridge D.G., Nguyen M., Kupplig S., Reth M., Shore G.C.;
 RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
 RT complex at the endoplasmic reticulum.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
 DR EMBL: AF422925; AAL87628.1;
 SQ SEQUENCE 538 AA; 61863 MW; 54402E6CAF9F6C9 CRC64;
 Query Match 9.8%; Score 128; DB: 4; Length 538;
 Best Local Similarity 27.3%; Pred. No. 0.023; 70; Indels 32; Gaps 6;
 Matches 48; Conservative 26; Mismatches 32; Indels 32; Gaps 6;
 QY 17 LGRRLDLARASPRTEGARRAGOPPLADPMDFELVY-----LHSYSSLSSETTEL 71
 DB 33 LGRRLDLARASPRTEGARRAGOPPLADPMDFELVY-----LHSYSSLSSETTEL 81
 QY 72 KRLCLGRVYKRLKLEVOGSLDFSMLENDLEPHTLRLSLARHDL-----R 126
 DB 82 KRLSLDYIPRKQEKIKALMLFQRLKRLLEESNLSTFLKLLRINLIDLLTYLNR 141
 QY 127 VDDFAGAAAGAPGEDICAFNYICDNVGRKMR-----LARQLVSDTKID 175
 DB 142 KEEMEREL---QTPGRAQI-SAYRYMLQISEEVSRLSKRFLQESISKID 193
 RESULT 5
 089110 PRELIMINARY; PRT: 480 AA.
 AC 089110; 035669;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CASPASE 8 precursor (EC 3.4.22.-) (CASPASE-8) (ICE-like apoptotic
 DE protease 5) (MORTI-associated CED-3 homolog) (MACH) (RADP-homologous
 DE ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine
 DE CASP8 OR CASP-8 OR FLICE.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-129/SV;
 RX MEDLINE-98316661; PubMed-9654089;
 RA Sakemai K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8.";
 RL Eur. J. Biochem. 253:399-405(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE-99057979; PubMed-9837723;
 RA Van de Craen M., Van Loc G., Declercq W., Schotte P., Fliers W.,
 RA van den Brande I., Mandruzzato S., van der Bruggen P., Fliers W.,
 RA Vandenberghe P.;
 RT "Molecular cloning and identification of murine caspase-8.";
 RL J. Mol. Biol. 284:1017-1026(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Struhsberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 57-476 FROM N.A.
 RA Submits P., Kischkel F., Poustka A., Kramer P.;
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
 CC TNF-1 INDUCED CELL DEATH. BINDING TO THE ADAPTER MOLECULE FADD
 CC RECRUITS IT TO EITHER RECEPTOR. THE RESULTING AGGREGATE CALLED THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
 CC LIBERATED FROM THE DISC AND ACTIVATES DOWNSTREAM APOPTOTIC
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIC
 CC (CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND
 CC ACTIVATES CASPASE-1, -2, -3, -6, -7, -8, -11/4 AND -12.

CC -1- FUNCTION: MAY PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS.
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP).
 CC HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-1-AMC
 CC (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INHIBITED BY Z-VAD-FK, CHMA AND P35.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC HIGHEST EXPRESSION IN SPLEEN, THYMUS, LUNG, LIVER AND KIDNEY.
 CC LOWER EXPRESSION IN HEART, BRAIN, TESTIS AND SKELETAL MUSCLE.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OCCURS AT
 CC DAY 7.
 CC -1- DOMAIN: CONTAINS TWO DEATH EFFECTOR DOMAINS (ALSO CALLED MORT
 CC MODULES) WHICH ARE INVOLVED IN THE BINDING OF CORRESPONDING
 CC SEQUENCE MOTIFS WITHIN FADD PROTEIN.
 CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC
 CC WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC
 CC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND CASPASE-10 CAN
 CC BE INVOLVED IN THESE PROCESSING EVENTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
 CC CASPASE FAMILY.
 DR EMBL: AF067841; AAC40132.1;
 DR EMBL: AF067835; AAC40132.1; JOINED.
 DR EMBL: AF067836; AAC40132.1; JOINED.
 DR EMBL: AF067837; AAC40132.1; JOINED.
 DR EMBL: AF067838; AAC40132.1; JOINED.
 DR EMBL: AF067839; AAC40132.1; JOINED.
 DR EMBL: AF067840; AAC40132.1; JOINED.
 DR EMBL: AF067834; AAC40131.1;
 DR EMBL: AJ007749; CAAC07677.1;
 DR EMBL: AJ000641; CAAC0196.1;
 DR EMBL: BC006737; AAH06737.1;
 DR HSP: O15806; 1009.
 DR MEROPS: C14_009;
 DR MGD: MGI:1261423; Casp8.
 DR InterPro: IPR001875; DEO.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF01335; DED; 2.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR SMART: SM00115; CASC; 1.
 DR SMART: SM00031; DED; 2.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS50168; DED; 2.
 KW Hydroxylase; Thiol protease; Apoptosis; zymogen.
 FT PROPEP 1 218
 FT CHAIN 1 218
 FT PROPEP 219 376
 FT CHAIN 219 376
 FT PROPEP 377 387
 FT CHAIN 377 387
 FT ACT_SITE 319 319
 FT ACT_SITE 319 319
 FT ACT_SITE 362 362
 FT DOMAIN 3 80
 FT DOMAIN 101 177
 FT CONFLICT 68 71
 FT CONFLICT 94 99
 FT CONFLICT 96 96
 FT CONFLICT 103 107
 FT CONFLICT 475 475
 FT CONFLICT 475 475
 SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5E4F CRC64;
 Query Match 9.6%; Score 125.5; DB 11; Length 480;
 Best Local Similarity 39.5%; Pred. No. 0.032;
 Matches 30; Conservative 13; Mismatches 32; Indels 1; Gaps 1;
 QY 49 MDPELVLAHSSVSSSELTEKLCGRVYKRLKLEVOGSLDFSMLENDLEPHT 108
 DB 1 MD-FOSCYAIADIELESSEDLAKLFQICLDIPHKQETLEDQKFLRLRGMLGEM 59
 QY 109 ELLRELLSLRHDL 124

Db 60 SFLKELFHISRDLL 75

RESULT 6

AC 09V3B4 PRELIMINARY; PRT; 239 AA.

DT 01-MAY-2000 (TEMBREL. 13, Last sequence update)

DT 01-JUN-2001 (TEMBREL. 17, Last annotation update)

DE C61297 protein (Death domain-containing adaptor protein).

GN B64 OR C61297.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_Taxid=7227;

RP SEQUENCE FROM N.A.

RC SRRAIN-BERKELEY;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Van K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Aroll J.F., Agbayani A., An H.-U., Andrews-Planckoch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evansgelist C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,

RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Malsbina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Sletten E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Strychar R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Zhou L., Steller H.;

RT "Bcl-2, a potential Drosophila homologue of FAS-associated death domain

RL containing protein (FADD)."

RN [3]

RP MEDLINE=20469420; PubMed=10934188;

RA Hu S., Yang X.;

RT "FADD, a Novel Death Domain-containing Adapter Protein for the

RL Drosophila Caspase DRSD."

DR J. Biol. Chem. 275:30761-30764(2000).

DR EMBL; AF003737; AAF55950.1;

DR EMBL; AF222005; AAF44325.1;

DR EMBL; AF295103; AAG22535.1;

DR Flybase; FBgn0038928; B64.

DR InterPro; IPR000488; Death.

DR Pfam; PF00531; death; 1.

DR SMART; SM00005; DEATH; 1.

DR PROSITE; P550017; DEATH DOMAIN; 1.

SO SEQUENCE 239 AA; 27421 MW; F43CFMA546C3FCD9 CRC64;

Query Match 9.4%; Score 122.5; DB 5; Length 239;

Best Local Similarity 20.8%; Pred. No. 0.022;

Matches 46; Conservative 44; Mismatches 70; Indels 61; Gaps 7;

Db 121 -----HDLLRRVDFE-----AGAAAGAPGEDLCA-----148

Qy 65 SSELFLKFLCLGRV-VKRLERVOGSLDFSLMLBQNDLEPHTLRELALSR---120

Db 21 TENVEDKLFLVEIGSGRRSDCTRTEDLDCLERADELSEYVEPLRISGMPOLE 80

Qy 149 -----FNVCNDVGRKWRRLARQLKVSDTKIDSTEDRYPNRLTERVESLR 194

Db 81 ALSATKRPENTLGHVNLVYELALAEELRQQLAIPASQNAQPSVSELAAPPTAIONY 140

Qy 141 ATPAAFTDKRTWFKKISELGRVYRRLGRSAGIGEGMDTEERYPHDLKSOI---LR 197

Db 195 IMKTERENA-----YVAHLVGLRSCQMLVADLVQVEYQ 230

Qy 198 LQLLEDDCHDPKHFLLRLCRALGDCGRN---DLKRRVQ 235

RESULT 7

AC 08TD11 PRELIMINARY; PRT; 171 AA.

DT 01-JUN-2002 (TEMBREL. 21, Created)

DT 01-JUN-2002 (TEMBREL. 21, Last sequence update)

DE 01-JUN-2002 (TEMBREL. 21, Last annotation update)

GN Procaspase-8 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=21927603; PubMed=11917123;

RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.,

RT "The procaspase-8 isoform, procaspase-8L, recruited to the Bap31

RL complex at the endoplasmic reticulum."

DR Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).

DR EMBL; AF422929; AA87632.1;

FT NON-TER 171 171

SO SEQUENCE 171 AA; 20361 MW; 5CBCA9EB5924CA9 CRC64;

Query Match 9.4%; Score 122; DB 4; Length 171;

Best Local Similarity 28.8%; Pred. No. 0.016;

Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

Qy 56 LHSVSSLSSESTELKFLCLGRVKKRLERVOGSLDFSLMLBQNDLEPHTLREL 115

Db 7 LYDIGEQLDSEDLASLKFSLDYTPQRKQEPIDALMLFRLQEKRLSESNLSFLKEL 66

Qy 116 ASLRRHDL-----RRYDDEAGAAAGAPGEDLCAFAVITCDNKKDKMR-----L 163

Db 67 FRINRDLALTYINTREKMEREL---QTGRRQI-SAYVMKYQISEVSRSELSFKF 122

Qy 164 ARQLKVSQTKID 175

Db 123 LLAQELSKCKLD 134

RESULT 8

Q96722

[illegible]

RESULT 9			
Q8TD13	Q8TD13	PRELIMINARY:	PRT: 339 AA.
ID	Q8TD13		
AC	Q8TD13:		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Procaspace-8 (Fragment).		
GN	CASP8.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21927603; PubMed-11917123;		
RA	Breckenridge D.G., Nguyen M., Kupfly S., Reth M., Shore G.C.;		
RT	"The procaspase-8 isoform, procaspase-8L, recruited to the BAP31		
RT	complex at the endoplasmic reticulum."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).		
DR	EMBL: AF429227; AL87630.1; -		
FT	NON_TER 339		
FT	NON_TER 339		
SEQ	SEQUENCE 339 AA: 39419 MW; 72FB2A620A5452B3 CRC64;		

	Query Match	Similarity	Score	IDB	Length
Best Local	28.8%	Pred. No. 0.039			
Matches	38	Conservative	23	Mismatches	55
				Indels	16
				Gaps	4

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	2	1	1
	3	1	1
	4	1	1
	5	1	1
	6	1	1
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	8	1	1
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	71	1	1
	72	1	1
	73	1	1
	74	1	1
	75	1	1
	76	1	1
	77	1	1
	78	1	1
	79	1	1
	80	1	1
	81	1	1
	82	1	1
	83	1	1
	84	1	1
	85	1	1
	86	1	1
	87	1	1
	88	1	1
	89	1	1
	90	1	1
	91	1	1
	92	1	1
	93	1	1
	94	1	1
	95	1	1
	96	1	1
	97	1	1
	98	1	1
	99	1	1
	100	1	1
	101	1	1
	102	1	1
	103	1	1
	104	1	1
	105	1	1
	106	1	1
	107	1	1
	108	1	1
	109	1	1
	110	1	1

RESULT 10			
Q8TD12	ID	Q8TD12	PRELIMINARY; PRT; 353 AA.
AC	Q8TD12		
DT	01-JUN-2002	(TREMBLrel. 21, Created)	
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	Procaspace-8 (Fragment).		
GN	CASP8.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_Taxid	9606;	
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE	21927603; PubMed	11917123;
RA	Breckenridge D.G., Nguyen M., Kuplig S., Rech M., Shore G.C.,		
RT	"The procaspase-8 isoform, procaspase-8L, recruited to the BAP31		
RL	complex at the endoplasmic reticulum."		
RL	Proc. Natl. Acad. Sci. U.S.A.	99:4331-4336	(2002).
DR	EMBL:	AF42928:	AA187631.1; -.
FT	NON_TER	353	
SQ	SEQUENCE	353 AA;	40905 MW; 797BB2998A8354FC CRC64;

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Query Match          9.48; Score 122; DB 4; Length 353;
Best Local Similarity 28.8%; Pred. No. 0.041;
Matches      38; Conservative 23; Mismatches 55; Indels 16; Gaps 4

QY 56 LHSVSSLSSELTETKEFLCIGRVYRKLEKRVSGIDLSMLEQNDLEPGHTELLRELL 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LYDIEQDSEDLASIKFLSLDIYIPQRKEPIKDALMLTFLQLEKRYLSENSLFLKELL 66
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 ASLRHDL-----RVYDFEAGAAAGAAGEDLCAAFVITCDNGKDKRR-----L 163
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 67 FRINLDLILITYLNTREKEMEREL---QTPGRAQI-SAYKVMLOYQISEVSRSELRSKFF 122
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 164 AROLKVPDKID 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 123 LIQEISTCKLD 134
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DR	EMBL	U50093	AA847805.1	JOINED
DR	EMBL	U50092	AA847805.1	JOINED
DR	EMBL	U50183	AA847805.1	
RT				complexity of pre-mRNA processing";
RT				Structure and organization of the human ankrylin-1 gene. Basis for
RA				Scarpie A.L., Lux S.E., Forget B.G.;
RA				Tse W.T., Scarpie A.L., Lux S.E., Forget B.G.;
RP				SEQUENCE FROM N.A.
RP				MEDLINE-91782244; PubMed-9235914;
OC				Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC				NCBI-Textid-9606;
OC				[1]
GN				ANK1.
GN				Homo sapiens (Human).
DE				01-JUN-2002 (TREMBlrel.. 21, last annotation update)
DE				Ankrylin.
DE				01-MAY-1997 (TREMBlrel.. 03, last sequence update)
DE				01-MAY-1997 (TREMBlrel.. 03, last sequence update)
AC				PRELIMINARY; PRT; 1656 AA.
AC				099407.
AC				099407.
RESULT 11				

DR EMBL: U50094; AAB47805.1; JOINED.
 DR EMBL: U50095; AAB47805.1; JOINED.
 DR EMBL: U50096; AAB47805.1; JOINED.
 DR EMBL: U50097; AAB47805.1; JOINED.
 DR EMBL: U50098; AAB47805.1; JOINED.
 DR EMBL: U50099; AAB47805.1; JOINED.
 DR EMBL: U50100; AAB47805.1; JOINED.
 DR EMBL: U50101; AAB47805.1; JOINED.
 DR EMBL: U50102; AAB47805.1; JOINED.
 DR EMBL: U50103; AAB47805.1; JOINED.
 DR EMBL: U50104; AAB47805.1; JOINED.
 DR EMBL: U50105; AAB47805.1; JOINED.
 DR EMBL: U50106; AAB47805.1; JOINED.
 DR EMBL: U50107; AAB47805.1; JOINED.
 DR EMBL: U50108; AAB47805.1; JOINED.
 DR EMBL: U50109; AAB47805.1; JOINED.
 DR EMBL: U50110; AAB47805.1; JOINED.
 DR EMBL: U50111; AAB47805.1; JOINED.
 DR EMBL: U50112; AAB47805.1; JOINED.
 DR EMBL: U50113; AAB47805.1; JOINED.
 DR EMBL: U50114; AAB47805.1; JOINED.
 DR EMBL: U50115; AAB47805.1; JOINED.
 DR EMBL: U50116; AAB47805.1; JOINED.
 DR EMBL: U50117; AAB47805.1; JOINED.
 DR EMBL: U50118; AAB47805.1; JOINED.
 DR EMBL: U50119; AAB47805.1; JOINED.
 DR EMBL: U50120; AAB47805.1; JOINED.
 DR EMBL: U50121; AAB47805.1; JOINED.
 DR EMBL: U50122; AAB47805.1; JOINED.
 DR EMBL: U50123; AAB47805.1; JOINED.
 DR EMBL: U50124; AAB47805.1; JOINED.
 DR EMBL: U50125; AAB47805.1; JOINED.
 DR EMBL: U50126; AAB47805.1; JOINED.
 DR EMBL: U50127; AAB47805.1; JOINED.
 DR EMBL: U50128; AAB47805.1; JOINED.
 DR EMBL: U50129; AAB47805.1; JOINED.
 DR EMBL: U50130; AAB47805.1; JOINED.
 DR EMBL: U50131; AAB47805.1; JOINED.
 DR EMBL: U50132; AAB47805.1; JOINED.
 DR HSSP: 000420; IARC.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000906; ZUS.
 DR Pfam: PF00023; ank; 23.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00791; ZUS; 1.
 DR PRINTS: PR01415; ANKRYIN.
 DR SMART: SM00248; ANK; 21.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00218; ZUS; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 20.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR ANK repeat: Repeat.
 SQ SEQUENCE 1856 AA; 203466 MW; 4A4E3A794DD6401F CRC64;

Query Match 9.3%; Score 121.5; DB 4; Length 1856;
 Best Local Similarity 27.2%; Pred. No. 0.4;
 Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;

OY 137 GAAGGEEEDICAAFNVCIDNVGKDWKRLAQLKVDKIDSIEDRPRNLTREVRSLRIW 196
 DB 1370 GSLGTGEGAEKMAVISRHGLSMAELARELOFVEDINRVRNPNLSLQSVALLIWM 1429
 OY 197 KNTKENATVAHLVGLRSCOMLVADLVQ-EVQOARDLQ-----NRSGAMSPKSNMSD 249
 DB 1430 VIRSGONAMNENTYALOSIDRGEIVNMLESGSGSRRLKFDRRRTDSDYSLSPQNMGY 1469
 OY 250 ASTSE 254
 DB 1490 SLIOD 1494

RESULT 12
 ID 08UVG5 PRELIMINARY; PRT; 418 AA.
 AC 08UVG5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Claprl.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OX Cyprinidae; Danio.
 NX NCBI_TaxID=7953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98021435; PubMed=9380701;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "Clarp, a death effector domain-containing protein interacts with
 RL caspase-8 and regulates apoptosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 RL zebrafish";
 RL Cell Death Differ. 7:509-510(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF448261; AAL41007.1;
 DR InterPro: IPR001875; DED.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF01335; DED; 1.
 DR SMART: SM00115; CASC; 1.
 DR SMART: SM00031; DED; 2.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS50168; DED; 2.
 SQ SEQUENCE 418 AA; 47619 MW; C2ECB3AE571E0237 CRC64;

Query Match 9.2%; Score 119.5; DB 13; Length 418;
 Best Local Similarity 25.6%; Pred. No. 0.083;
 Matches 54; Conservative 35; Mismatches 83; Indels 39; Gaps 8;

OY 2 NQAPCEFRGGGILGPL--GKRRDLA---ASEPRFGARRAGQPPLADPAMPDELY 54
 DB 53 NQAGPHSGNALLMELMGMKRYDLKRVPTNQQVGIAR---KEVID-----YRV 104
 OY 55 LHSVSSLSSELTTELKFCIGRVYKRLERVOGDLFEMLEQNDLEFGHTELLREL 114
 DB 105 LMADVSEMLDEKEDLSLFLLSLIPKERSYRAVSFLDYVVELEKLNSEKDLFEKC 164
 OY 115 LASLRHDLRRVDFEAGAAGAAGEEDICAFNVT-----CDNVGKDWKRL----- 163
 DB 165 LKNIIRNDLVAKIQAYR-----NRGQNMCAAPNITKFTPMQCPPEKQVRSQCFNH 217
 OY 164 ---ARQLKVSPTKI---DSIEDRYPRNLTRE 188
 DB 218 EFNKLKLSVPTGHIYQQAITEEQMNEQR 248
 RESULT 13
 ID 013768 PRELIMINARY; PRT; 1719 AA.
 AC 013768;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alt. ankyrin (variant 2.2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=HEMATOPOIETIC;
RC MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.
RL Nature 344:36-42(1990).
DR EMBL: X16603; CA34611.1;
DR HSSP: Q00420; IAWC.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000906; ZUS.
DR Pfam: PF000531; ank; 24.
DR Pfam: PF00531; death; 1.
DR PRINTS: PRO1415; ANKYRIN.
DR SMART: SM00248; ANK; 22.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00218; ZUS; 1.
DR PROSITE: PS50086; ANK_REPEAT; 20.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1719 AA; 189011 MW; F63465D16D975CBF CRC64;

Query Match 9.18; Score 118.5; DB 4; Length 1719;
Best Local Similarity 28.08; Pred. No. 0.64;
Matches 33; Conservative 26; Mismatches 52; Indels 7; Gaps 2;

OY 137 GAAPGEEDLCAAFNVICDNGKMDRRRLAROLKYSDFITSDIEDRYPNLTERRESLRIN 196
DB 1395 GSISGTEQAKMAKVAISEHGLSMAELAKELQSVEDINIRVENPNSLQSYALNTLW 1454
OY 197 KNTKENATVAVHVGALRSCQNNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWN 247
DB 1455 VIREGQVANNENLYTALQSIDRGIVNMLGSGRQSNLKPDRHRTDROYSLSFSQKN 1512

RESULT 14
OY 063128 PRELIMINARY; PRT; 941 AA.
AC 063128;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Cpe2 protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HIPPOCAMPAL DENTATE GYRUS;
RC MEDLINE=96312537; PubMed=8700883;
RA Nedivi E., Fellust S., Theill L., Heyvront D.;
RT "A set of genes expressed in response to light in the adult cerebral
RT cortex and regulated during development.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2048-2053(1996).
DR EMBL: X95466; CA64740.1;
DR InterPro: IPR002017; Spectrin.
SQ SEQUENCE 941 AA; 109037 MW; EC50B042E22AF4248 CRC64;

Query Match 9.18; Score 118; DB 11; Length 941;
Best Local Similarity 22.78; Pred. No. 0.32;
Matches 58; Conservative 47; Mismatches 96; Indels 54; Gaps 11;

OY 11 GILGPIGKR---DLARSEPTEGARRAGQPRPADPMDPVLVLLHSVSSLS- 65

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DB 678 GELLSMLKSLKRLIDVSSNE-----AQRGDELAELS-SKALVALLSEVEKMLSNF 731
OY 66 SETLEKFLICIGHYVKKTERVOG-----LDLSMLLEQNDLBERGHTELRE-----LIAS 117
DB 732 GECVOYK-----EIVSSLEGLMSGSESDAEFTIDTENTLEAQQMLLRHOKFTMIS 786
OY 118 LRRHDLIRVYDDEAGAGAPGEEDLCAAFNVICDNGKMDRRRLAROLKYSDFITSDI 177
DB 787 AKRRDLQQQEQGCGGQAG--PGQEL-----RKLESTLTGLDGS 825
OY 178 EDRTYPRNLTFRVRESIRIKNTKENTVAHV-----GALRSCQNNLVADLVQEVQOAR 232
DB 826 REQOER---RIVQSLKMERFEFNKTVVRLVFQSGSSHERLFSLSLSSELRQTK 881
OY 233 DLQNRSGAMSPMSWN 247
DB 882 EFSKTESINATQAEEN 896

RESULT 15
OY 061302 PRELIMINARY; PRT; 1848 AA.
AC 061302;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Erythroid ankyrin.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=NEURAL;
RC MEDLINE=93252825; PubMed=8486643;
RA Barker J.E.;
RA Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RT "Complex patterns of sequence variation and multiple 5' and 3' ends
RT are found among transcripts of the erythroid ankyrin gene.";
RL J. Biol. Chem. 268:9533-9540(1993).
DR EMBL: X69063; CA46801.1;
DR HSSP: Q00420; IAWC.
DR MGD: MGI:88024; ANK1.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000906; ZUS.
DR Pfam: PF000531; ank; 24.
DR Pfam: PF00531; death; 1.
DR PRINTS: PRO1415; ANKYRIN.
DR SMART: SM00248; ANK; 22.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00218; ZUS; 1.
DR PROSITE: PS50086; ANK_REPEAT; 20.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1848 AA; 202577 MW; 5744BECBF9EBA056 CRC64;

Query Match 9.08; Score 117.5; DB 11; Length 1848;
Best Local Similarity 27.98; Pred. No. 0.85;
Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;

OY 151 VICDNGKMDRRRLAROLKYSDFITSDIEDRYPNLTERRESLRINNTKENTVAHV 210
DB 1421 VIREHGLSMAELAKELQSVEDINIRVENPNSLQSYALNTLWVDRBEGENAKMENTLY 1480
OY 211 GALSRCQNNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWDASTS 254
DB 1481 TALNIDRSEIVNMLEVSGRQSNLKPDRHRTDROYSLSFSQKN 1531

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Thu Jun 19 11:26:31 2003

Search completed: June 19, 2003, 10:38:43.
Job time : 83 secs

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